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(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE
SAME

FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.
25 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and
30

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

- 5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

- 10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

- In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

- In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

5 nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

10 In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80 % nucleic acid sequence identity, alternatively at least about 81 % nucleic acid sequence identity, alternatively at least about 82 % nucleic acid sequence identity, alternatively at least about 83 % nucleic acid sequence identity, alternatively at least about 84 % nucleic acid sequence identity, alternatively at least about 85 % nucleic acid sequence identity, alternatively at least about 86 % nucleic acid sequence identity, alternatively at least about 87 % nucleic acid sequence identity, alternatively at least about 88 % nucleic acid sequence identity, alternatively at least about 89 % nucleic acid sequence identity, alternatively at least about 90 %
15 nucleic acid sequence identity, alternatively at least about 91 % nucleic acid sequence identity, alternatively at least about 92 % nucleic acid sequence identity, alternatively at least about 93 % nucleic acid sequence identity, alternatively at least about 94 % nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

20 Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

25 Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length,
30 alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO276 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16435-1208".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO284 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA23318-1211".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO193 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA23322-1393".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO190 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA23334-1392".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO180 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA26843-1389".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO194 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA26844-1394".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO218 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA30867-1335".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO260 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA33470-1175".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO233 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA34436-1238".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO234 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA35557-1137".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO236 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA35599-1168".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO244 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA35668-1171".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO262 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA36992-1168".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO271 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA39423-1182".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO268 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA39427-1179".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO270 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA39510-1181".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO355 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA39518-1247".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO298 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA39975-1210".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO299 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA39976-1215".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO296 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA39979-1213".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO329 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA40594-1233".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO330 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA40603-1232".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO294 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA40604-1187".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO300 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA40625-1189".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO307 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA41225-1217".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO334 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA41379-1236".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO352 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA41386-1316".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO710 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA44161-1434".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO873 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA44179-1362".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO354 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA44192-1246".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA44694-1500".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO382 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA45234-1277".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA45409-2511".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO386 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA45415-1318".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO541 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA45417-1432".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO852 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA45493-1349".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO700 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA46776-1284".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figures 75A-75B show a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO708 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA48296-1292".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figures 75A-75B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO707 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA48306-1291".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO864 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA48328-1355".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO706 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA48329-1290".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO732 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA48334-1435".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO537 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA49141-1431".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO545 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA49624-1279".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO718 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA49647-1398".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO872 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA49819-1439".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO704 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA50911-1288".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO705 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA50914-1289".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO871 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA50919-1361".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO702 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA50980-1286".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO944 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA52185-1370".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO739 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA52756".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO941 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA53906-1368".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA53912-1457".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA53913-1490".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO983 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA53977-1371".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO784 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA53978-1443".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO783 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA53996-1442".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO940 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA54002-1367".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO768 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA55737-1345".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA56050-1455".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA56052-1454".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1018 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA56107-1415".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO793 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA56110-1437".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA56406-1704".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA56409-1377".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA56410-1414".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO937 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA56436-1448".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56529-1647".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO842 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56855-1447".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO839 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56859-1445".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56860-1510".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA56865-1491".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA56868-1478".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA56869-1545".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA56870-1492".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO827 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA57039-1402".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA57253-1382".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1113 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA57254-1477".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA57699-1412".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA57704-1452".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA57710-1451".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA57827-1493".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

10 Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA57844-1410".

Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA58723-1588".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA58727-1474".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA58730-1607".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA58732-1650".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA58737-1473".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA58743-1609".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA58747-1384".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA58828-1519".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA58846-1409".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA58848-1472".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA58849-1494".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA58850-1495".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA58852-1637".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA58853-1423".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO994 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA58855-1422".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA59211-1450".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA59212-1627".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA59213-1487".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA59219-1613".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA59497-1496".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA59602-1436".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA59603-1419".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA59605-1418".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA59607-1497".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA59610-1556".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA59612-1466".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA59613-1417".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA59616-1465".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA59619-1464".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA59625-1498".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA59817-1703".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA59827-1426".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA59828-1608".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA59837-2545".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA59844-2542".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA59853-1505".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA59854-1459".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA59855-1485".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA60278-1530".

15 Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA60283-1484".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

20 Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA60608-1577".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

25 Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO1197 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA60611-1524".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA60619-1482".

30 Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA60625-1507".

35 Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA60629-1481".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA60740-1615".

5 Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA61608-1606".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

10 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA61755-1554".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

15 Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA62809-1531".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA62812-1594".

20 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA62813-2544".

25 Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA62845-1684".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

30 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA64849-1604".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

35 Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA64852-1589".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA64863-1573".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

5 Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA64881-1602".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA64902-1667".

10 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA64952-1568".

15 Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA65403-1565".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

20 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA65413-1534".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

25 Figures 289A-289B show a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA65423-1595".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figures 289A-289B.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA66304-1546".

30 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA66308-1537".

35 Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA66511-1563".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA66512-1564".

5 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA66519-1535".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

10 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA66521-1583".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

15 Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA66658-1584".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA66660-1585".

20 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA66669-1597".

25 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA66674-1599".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

30 Figures 311A-311B show a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA68836-1656".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figures 311A-311B.

35 Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA68862-2546".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA68866-1644".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

5 Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA68869-1610".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA68871-1638".

10 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA68879-1631".

15 Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA68880-1676".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

20 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA68882-1677".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

25 Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA68883-1691".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA68885-1678".

30 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA68886".

35 Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA71180-1655".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA71184-1634".

5 Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA71213-1659".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

10 Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA71234-1651".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

15 Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA71269-1621".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA71277-1636".

20 Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA71286-1687".

25 Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA71883-1660".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

30 Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA73401-1633".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

35 Figures 351A-351B show a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA73492-1671".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figures 351A-351B.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA73730-1679".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

5 Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA73734-1680".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA73735-1681".

10 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA73742-1662".

15 Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA73746-1654".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

20 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA73760-1672".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

25 Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA76393-1664".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA76398-1699".

30 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA76399-1700".

35 Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA76522-2500".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA76533-1689".

5 Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA77303-2502".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

10 Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA77626-1705".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

15 Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA77648-1688".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA81754-2532".

20 Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA81757-2512".

25 Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA82302-2529".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

30 Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA82340-2530".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

35 Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA83551".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA87991-2540".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

5 Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA88002".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA92238-2539".

10 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA95930".

15 Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA115291-2681".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

20 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA23336-2861".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

25 Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO203 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA30862-1396".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO204 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA30871-1157".

30 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO210 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA32279-1131".

35 Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO223 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA33206-1165".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO247 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA35673-1201".

5 Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO358 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA47361-1154-2".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

10 Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO724 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA49631-1328".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

15 Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO868 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA52594-1270".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO740 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA55800-1263".

20 Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56531-1648".

25 Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO162 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56965-1356".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

30 Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO828 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA57037-1444".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

35 Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO819 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57695-1340".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO813 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57834-1339".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

5 Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57841-1522".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO887 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA58130".

10 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA58847-1383".

15 Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA59493-1420".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

20 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59586-1520".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

25 Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59608-2577".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59849-1504".

30 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA60292-1506".

35 Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA62377-1381-1".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA62880-1513".

5 Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA66672-1586".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

10 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA67962-1649".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

15 Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA69555-2867".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA71162-2764".

20 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA71290-1630".

25 Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA76401-1683".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

30 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA76541-1675".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

35 Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA76788-2526".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA77623-2524".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

5 Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA80136-2503".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

10 Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA83568-2692".

Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA84210-2576".

15 Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA86576-2595".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

20 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA87976-2593".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

25 Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA92256-2596".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA92289-2598".

30 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA96850-2705".

35 Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA96855-2629".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA96857-2636".

5 Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA96860-2700".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

10 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA96861-2844".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

15 Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA96866-2698".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA96870-2676".

20 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA96872-2674".

25 Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA96878-2626".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

30 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA96879-2619".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

35 Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA96889-2641".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA96893-2621".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

5 Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA96897-2688".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA98564-2643".

10 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA107443-2718".

15 Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA107786-2723".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

20 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA108682-2712".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

25 Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA108684-2761".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA108701-2749".

30 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA108720-2717".

35 Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA108726-2729".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figures 525A-525B show a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA108728-2760".

5 Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figures 525A-525B.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA108738-2767".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

10 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA108743-2722".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

15 Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA108758-2759".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA108765-2758".

20 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA108783-2747".

25 Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA108789-2748".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

30 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA108806-2724".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

35 Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA108936-2719".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA119510-2771".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

5 Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA119517-2778".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA119535-2756".

10 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA119537-2777".

15 Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA119714-2851".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

20 Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA125170-2780".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

25 Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA129594-2841".

Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA129793-2857".

30 Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA130809-2769".

35 Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

Figure 561 shows a nucleotide sequence (SEQ ID NO:561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:561 is a clone designated herein as "DNA131639-2874".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561 shown in Figure 561.

Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA131649-2855".

5 Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA131652-2876".

Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

10 Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA131658-2875".

Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

15 Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA132162-2770".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA136110-2763".

20 Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA139592-2866".

25 Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA139608-2856".

Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

30 Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA143292-2848".

Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

35 Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA144844-2843".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA144857-2845".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

5 Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA145841-2868".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA148004-2882".

10 Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA149893-2873".

15 Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA149930-2884".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

20 Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA150157-2898".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

25 Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA150163-2842".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA153579-2894".

30 Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA164625-2890".

35 Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO791 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA57838-1337".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA59777-1480".

5 Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA66675-1587".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

10 Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA76532-1702".

Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

15 Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA105849-2704".

Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA83500-2506".

20 Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

25 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein
30 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO
35 polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as

the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO

polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through

Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the

National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent

different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions,

to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

5 "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic
10 uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one
15 component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated
20 polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of
25 natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

25 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked"
30 means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

35 The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially

homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding

specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

5 "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an
10 antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically
15 include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

20 "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

30 Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable
35 carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine,

asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

5 "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

10 Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

15 The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

20 The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

30 "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

35 The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same

polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

5 An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence
10 by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

15 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical
20 alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay
25 plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of
30 biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.
35

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
5  * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M      -8      /* value of a match with a stop */

10 int      _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ { -2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ { -4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ { -1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ { -1, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ { -1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ { -2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ { -1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ { -2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ { -6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ { -3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};
40
45
50
55

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
#define DINS1         1      /* penalty per base */
#define PINS0         8      /* penalty for a gap */
#define PINS1         4      /* penalty per residue */

struct jmp {
    short      n[MAXJMP];    /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
    int      score;          /* score at last jmp */
    long     offset;         /* offset of prev block */
    short    ijmp;           /* current jmp index */
    struct jmp jp;           /* list of jmps */
};

struct path {
    int      spc;             /* number of leading spaces */
    short    n[JMPS]; /* size of jmp (gap) */
    int      x[JMPS]; /* loc of jmp (last elem before gap) */
};

char      *ofile;           /* output file name */
char      *namex[2];        /* seq names: getseqs() */
char      *prog;            /* prog name for err msgs */
char      *seqx[2];         /* seqs: getseqs() */
int      dmax;              /* best diag: nw() */
int      dmax0;             /* final diag */
int      dna;               /* set if dna: main() */
int      endgaps;           /* set if penalizing end gaps */
int      gapx, gapy;        /* total gaps in seqs */
int      len0, len1;        /* seq lens */
int      ngapx, ngapy;      /* total size of gaps */
int      smax;              /* max score: nw() */
int      *xbm;              /* bitmap for matching */
long     offset;           /* current offset in jmp file */
struct    diag dx;          /* holds diagonals */
struct    path pp[2];       /* holds path for seqs */

char      *calloc(), *malloc(), *index(), *strcpy();
char      *getseq(), *g_calloc();

```

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
*   where file1 and file2 are two dna or two protein sequences.
5  * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
20 };

static _pbval[26] = {
    1, 2|(1<(<('D'-'A'))|(1<(<('N'-'A'))), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<(<10, 1<(<11, 1<(<12, 1<(<13, 1<(<14,
25 1<(<15, 1<(<16, 1<(<17, 1<(<18, 1<(<19, 1<(<20, 1<(<21, 1<(<22,
    1<(<23, 1<(<24, 1<(<25|(1<(<('E'-'A'))|(1<(<('Q'-'A'))
    );

main(ac, av)
30     int    ac;
    char    *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';', '>' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0;                /* 1 to penalize endgaps */
    ofile = "align.out";        /* output file */

50     nw();                    /* fill in the matrix, get the possible jumps */
    readjumps();                /* get the actual jumps */
    print();                    /* print stats, alignment */

55     cleanup(0);              /* unlink any tmp files */
}

```

main

Table 1 (cont')

```

/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()
{
    10      char      *px, *py;      /* seqs and ptrs */
        int      *ndely, *dely;    /* keep track of dely */
        int      ndelx, delx;      /* keep track of delx */
        int      *tmp;            /* for swapping row0, row1 */
        int      mis;            /* score for each type */
    15      int      ins0, ins1;    /* insertion penalties */
        register id;             /* diagonal index */
        register ij;            /* jmp index */
        register *col0, *col1;    /* score for curr, last row */
        register xx, yy;         /* index into seqs */

    20      dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    25      col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

    30      smax = -10000;
        if (endgaps) {
            for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                col0[yy] = dely[yy] = col0[yy-1] - ins1;
                ndely[yy] = yy;
    35            }
            col0[0] = 0;      /* Waterman Bull Math Biol 84 */
        }
        else
            for (yy = 1; yy <= len1; yy++)
    40                dely[yy] = -ins0;

        /* fill in match matrix
        */
    45      for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (endgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
    50            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
    55            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
    60

```

Table 1 (cont')

...nw

```

5      for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

        /* update penalty for del in x seq;
        * favor new del over ongong del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
            if (col0[yy] - ins0 >= dely[yy]) {
15                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
20            }
        } else {
            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
25            } else
                ndely[yy]++;
        }

        /* update penalty for del in y seq;
        * favor new del over ongong del
        */
        if (endgaps || ndelx < MAXGAP) {
            if (col1[yy-1] - ins0 >= delx) {
35                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else {
                delx -= ins1;
                ndelx++;
40            }
        } else {
            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
45            } else
                ndelx++;
        }

        /* pick the maximum score; we're favoring
        * mis over any del and delx over dely
        */
50
55
60

```

Table 1 (cont')

...nw

```

5      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          coll[yy] = mis;
      else if (delx >= dely[yy]) {
          coll[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
15      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = ndelx;
          dx[id].jp.x[ij] = xx;
          dx[id].score = delx;
20      }
      else {
          coll[yy] = dely[yy];
          ij = dx[id].ijmp;
25      if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
          && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINSO)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
30      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = -ndely[yy];
          dx[id].jp.x[ij] = xx;
          dx[id].score = dely[yy];
35      }
      if (xx == len0 && yy < len1) {
          /* last col
           */
          if (endgaps)
              coll[yy] -= ins0+ins1*(len1-yy);
          if (coll[yy] > smax) {
45      smax = coll[yy];
              dmax = id;
          }
      }
50      if (endgaps && xx < len0)
          coll[yy-1] -= ins0+ins1*(len0-xx);
      if (coll[yy-1] > smax) {
          smax = coll[yy-1];
          dmax = id;
55      }
      tmp = col0; col0 = coll; coll = tmp;
  }
  (void) free((char *)ndely);
  (void) free((char *)dely);
  (void) free((char *)col0);
  (void) free((char *)coll);
60      }

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3 /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "< first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "< second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
55         lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```


Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int      lx, ly;
    int      firstgap, lastgap;
    /* "core" (minus endgaps) */
    /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
10    char     outx[32];
    double   pct;
    register n0, n1;
    register char *p0, *p1;

15    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25         if (siz0) {
             p1++;
             n1++;
             siz0--;
         }
         else if (siz1) {
30             p0++;
             n0++;
             siz1--;
         }
         else {
35             if (xbm[*p0-'A']&xbm[*p1-'A'])
                 nm++;
             if (n0++ == pp[0].x[i0])
40                 siz0 = pp[0].n[i0++];
             if (n1++ == pp[1].x[i1])
                 siz1 = pp[1].n[i1++];
             p0++;
             p1++;
         }
45     }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

Table 1 (cont')

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, "(%d %s%s)",
        ngapx, (dna)? "base": "residue", (ngapx == 1)? "": "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, "(%d %s%s)",
            ngapy, (dna)? "base": "residue", (ngapy == 1)? "": "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base": "residue", (firstgap == 1)? "": "s",
            lastgap, (dna)? "base": "residue", (lastgap == 1)? "": "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

static nm;          /* matches in core -- for checking */
static lmax;        /* lengths of stripped file names */
static ij[2];       /* jmp index for a path */
static nc[2];        /* number at start of current line */
static ni[2];        /* current elem number -- for gapping */
static siz[2];
static char *ps[2];   /* ptr to current element */
static char *po[2];   /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int nm;          /* char count */
    int more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nm = stripname(namex[i]);
        if (nm > lmax)
            lmax = nm;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

5   for (nn = nm = 0, more = 1; more;) {
        for (i = more = 0; i < 2; i++) {
            /*
            * do we have more of this sequence?
            */
            if (!*ps[i])
                continue;

10          more++;

            if (pp[i].spc) { /* leading space */
                *po[i]++ = ' ';
                pp[i].spc--;
15          }
            else if (siz[i]) { /* in a gap */
                *po[i]++ = '-';
                siz[i]--;
20          }
            else { /* we're putting a seq element
                */
                *po[i] = *ps[i];
                if (islower(*ps[i]))
                    *ps[i] = toupper(*ps[i]);
25                po[i]++;
                ps[i]++;

                /*
                * are we at next gap for this seq?
                */
                if (ni[i] == pp[i].x[ij[i]]) {
                    /*
                    * we need to merge all gaps
                    * at this location
                    */
                    siz[i] = pp[i].n[ij[i]++];
                    while (ni[i] == pp[i].x[ij[i]])
                        siz[i] += pp[i].n[ij[i]++];
35                }
                ni[i]++;
40          }
        }
        if (++nn == olen || !more && nn) {
            dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
            nn = 0;
50    }
    }

    /*
    * dump a block of lines, including numbers, stars: pr_align()
    */
55    static
    dumpblock()
    {
        register i;

60        for (i = 0; i < 2; i++)
            *po[i]-- = '\0';
    }

```

...pr_align

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void) putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10             putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15             }
          }
      }

/*
20  * put out a number line: dumpblock()
  */
static
nums(ix)                                nums
25  {
      int      ix;      /* index in out[] holding seq line */

      char      nline[P_LINE];
      register  i, j;
      register char *pn, *px, *py;

30      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
          if (*py == ' ' || *py == '-')
              *pn = ' ';
35          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
                  for (px = pn; j /= 10, px--)
                      *px = j%10 + '0';
40                  if (i < 0)
                      *px = '-';
              }
              else
                  *pn = ' ';
45              i++;
          }
      }
      *pn = '\0';
      nc[ix] = i;
50      for (pn = nline; *pn; pn++)
          (void) putc(*pn, fx);
      (void) putc('\n', fx);
  }

55  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
static
putline(ix)                                putline
60      int      ix;      {

```

Table 1 (cont')

```

...putline
5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
10         (void) putc(' ', fx);

      /* these count from 1:
      * ni[] is current element (from 1)
      * nc[] is number at start of current line
      */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
    }

20     /*
     * put a line of stars (seqs always in out[0], out[1]): dumpblock()
     */
    static
25     stars()
    {
        int          i;
        register char *p0, *p1, cx, *px;

30         if (!*out[0] || (*out[0] == ' ' && *p0 == ' ') ||
            !*out[1] || (*out[1] == ' ' && *p1 == ' '))
            return;
        px = star;
35         for (i = lmax+P_SPC; i; i--)
            *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
            if (isalpha(*p0) && isalpha(*p1)) {
40                 if (xbm[*p0-'A']&xbm[*p1-'A']) {
                    cx = '*';
                    nm++;
                }
                else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                     cx = '.';
                else
                    cx = ' ';
            }
            else
50                 cx = ' ';
            *px++ = cx;
        }
        *px++ = '\n';
55     *px = '\0';
    }

60

```

stars

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;
10     py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
15     if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
20
25
30
35
40
45
50
55
60

```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_alloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps; from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>
10
char    *jname = "/tmp/homgXXXXXX";    /* tmp file for jumps */
FILE    *fj;

int      cleanup();                    /* cleanup tmp file */
15 long    lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)                                cleanup
{
    int    i;
    if (fj)
        (void) unlink(jname);
25    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
30 getseq(file, len)                                getseq
{
    char    *file;    /* file name */
    int     *len;     /* seq len */
35
    {
        char    line[1024], *pseq;
        register char    *px, *py;
        int     natgc, tlen;
        FILE    *fp;
40
        if ((fp = fopen(file, "r")) == 0) {
            fprintf(stderr, "%s: can't read %s\n", prog, file);
            exit(1);
45        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
            if (*line == ';' || *line == '<' || *line == '>')
                continue;
            for (px = line; *px != '\n'; px++)
                if (isupper(*px) || islower(*px))
                    tlen++;
50        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
            fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
            exit(1);
55        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

```

5      py = pseq + 4;
      *len = tlen;
      rewind(fp);

      while (fgets(line, 1024, fp)) {
          if (*line == ';' || *line == '<' || *line == '>')
              continue;
          for (px = line; *px != '\n'; px++) {
10             if (isupper(*px))
                 *py++ = *px;
             else if (islower(*px))
                 *py++ = toupper(*px);
             if (index("ATGCU", *(py-1)))
15                 natgc++;
          }
          *py++ = '\0';
          *py = '\0';
          (void) fclose(fp);
          dna = natgc > (tlen/3);
          return(pseq+4);
      }

25  char *
      g_alloc(msg, nx, sz)
          char *msg;          /* program, calling routine */
          int nx, sz;         /* number and size of elements */
      {
30          char *px, *calloc();

          if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
              if (*msg) {
35                  fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                  exit(1);
              }
          }
          return(px);
      }

40  /*
      * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
      */
      readjmps()
45  {
          int fd = -1;
          int siz, i0, i1;
          register i, j, xx;

50          if (fj) {
              (void) fclose(fj);
              if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                  fprintf(stderr, "%s: can't open() %s\n", prog, jname);
                  cleanup(1);
55              }
          }
          for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
              while (1) {
60                  for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                      ;
            
```

...getseq

g_alloc

readjmps

Table 1 (cont')

...readjumps

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
            break;
10    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20            pp[1].n[i1] = -siz;
            xx += siz;
            /* id = xx - yy + len1 - 1
            */
            pp[1].x[i1] = xx - dmax + len1 - 1;
            gapy++;
            ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30        }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
40        }
    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
        offset = 0;
60    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int      ix;
    {
        char  *mktemp();
10     if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15     if ((fj = fopen(jname, "w")) == 0) {
                fprintf(stderr, "%s: can't write %s\n", prog, jname);
                exit(1);
            }
20     (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }

25

30

35

40

45

50

55

60

```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
15 Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

20

5 divided by 10 = 50%

Table 4

25

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

20 As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

30 In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35 Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO
15 polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., **13**:4331 (1986); Zoller et al., Nucl. Acids Res., **10**:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

5 Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1
10 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane
15 and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.
25

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.
30

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding
35

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., **85**:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan'*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan'*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilae* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* 15 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not 20 limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant 25 cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, 30 ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as
10 signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

15 Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for
20 cloning vectors in mammalian cells.

 Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a
30 selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

 Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well
35 known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

5 Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

10 Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

15 PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

20 Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

25 Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

30 Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding

naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an

antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

5 Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or
10 receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

15 Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

20 The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome
25 using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified.
30 Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules
35 contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional

gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane.

5 (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

25 The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

30 The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

35 The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient

having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, PLURONICSTM or PEG.

10 The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

15 The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

20 Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

25 When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

30 Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon- (rhIFN-), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit

and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582

(1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single

clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA.

Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

F. Anti-PRO Antibodies

15 The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

35 The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or

lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding

sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

10 *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

15 The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a
20 complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially
25 all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*,
30 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No.

4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least

one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large
10 amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical
15 linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar
20 amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to
25 directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers.
30 Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for
35 making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary

V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, *J. Immunol.* 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, *J. Immunol.* 147:60 (1991).

5 Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic
10 agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

15 Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example,
20 immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

6. Effector Function Engineering

25 It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, *J. Exp Med.*, 176:
30 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design,
35 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent

such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified

by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

5 Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

10 Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current
15 Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized
20 appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

25 1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA
30 was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

35 A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linkered with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2×10^6 cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10^7 cells/ml (approx. OD₆₀₀=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μ g, vol. < 10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l Klentaq (Clontech, Palo Alto, CA); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:611)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:612)

PCR was then performed as follows:

- | | | |
|----|--------------|------------------|
| a. | Denature | 92°C, 5 minutes |
| b. | 3 cycles of: | |
| | Denature | 92°C, 30 seconds |
| | Anneal | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA16435-1208	209930	June 2, 1998
	DNA23318-1211	209787	April 21, 1998
	DNA23322-1393	203400	October 27, 1998
5	DNA23334-1392	209918	June 2, 1998
	DNA26843-1389	203099	August 4, 1998
	DNA 26844-1394	209926	June 2, 1998
	DNA30867-1335	209807	April 28, 1998
	DNA33470-1175	209398	October 17, 1997
10	DNA34436-1238	209523	December 10, 1997
	DNA35557-1137	209255	September 16, 1997
	DNA35599-1168	209373	October 16, 1997
	DNA35668-1171	209371	October 16, 1997
	DNA36992-1168	209382	October 16, 1997
15	DNA39423-1182	209387	October 17, 1997
	DNA39427-1179	209395	October 17, 1997
	DNA39510-1181	209392	October 17, 1997
	DNA39518-1247	209529	December 10, 1997
	DNA39975-1210	209783	April 21, 1998
20	DNA39976-1215	209524	December 10, 1997
	DNA39979-1213	209789	April 21, 1998
	DNA40594-1233	209617	February 5, 1998
	DNA40603-1232	209486	November 21, 1997
	DNA40604-1187	209394	October 17, 1997
25	DNA40625-1189	209788	April 21, 1998
	DNA41225-1217	209491	November 21, 1997
	DNA41379-1236	209488	November 21, 1997
	DNA41386-1316	209703	March 26, 1998
	DNA44161-1434	209907	May 27, 1998
30	DNA44179-1362	209851	May 6, 1998
	DNA44192-1246	209531	December 10, 1997
	DNA44694-1500	203114	August 11, 1998
	DNA45234-1277	209654	March 5, 1998
	DNA45409-2511	203579	January 12, 1999
35	DNA45415-1318	209810	April 28, 1998
	DNA45417-1432	209910	May 27, 1998
	DNA45493-1349	209805	April 28, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA46776-1284	209721	March 31, 1998
	DNA48296-1292	209668	March 11, 1998
	DNA48306-1291	209911	May 27, 1998
5	DNA48328-1355	209843	May 6, 1998
	DNA48329-1290	209785	April 21, 1998
	DNA48334-1435	209924	June 2, 1998
	DNA49141-1431	203003	June 23, 1998
	DNA49624-1279	209655	March 5, 1998
10	DNA49647-1398	209919	June 2, 1998
	DNA49819-1439	209931	June 2, 1998
	DNA50911-1288	209714	March 31, 1998
	DNA50914-1289	209722	March 31, 1998
	DNA50919-1361	209848	May 6, 1998
15	DNA50980-1286	209717	March 31, 1998
	DNA52185-1370	209861	May 14, 1998
	DNA53906-1368	209747	April 7, 1998
	DNA53912-1457	209870	May 14, 1998
	DNA53913-1490	203162	August 25, 1998
20	DNA53977-1371	209862	May 14, 1998
	DNA53978-1443	209983	June 16, 1998
	DNA53996-1442	209921	June 2, 1998
	DNA54002-1367	209754	April 7, 1998
	DNA55737-1345	209753	April 7, 1998
25	DNA56050-1455	203011	June 23, 1998
	DNA56052-1454	203026	June 23, 1998
	DNA56107-1415	203405	October 27, 1998
	DNA56110-1437	203113	August 11, 1998
	DNA56406-1704	203478	November 17, 1998
30	DNA56409-1377	209882	May 20, 1998
	DNA56410-1414	209923	June 2, 1998
	DNA56436-1448	209902	May 27, 1998
	DNA56529-1647	203293	September 29, 1998
	DNA56855-1447	203004	June 23, 1998
35	DNA56859-1445	203019	June 23, 1998
	DNA56860-1510	209952	June 9, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA56868-1478	203024	June 23, 1998
	DNA56869-1545	203161	August 25, 1998
	DNA56870-1492	209925	June 2, 1998
5	DNA57039-1402	209777	April 14, 1998
	DNA57253-1382	209867	May 14, 1998
	DNA57254-1477	203289	September 29, 1998
	DNA57699-1412	203020	June 23, 1998
	DNA57704-1452	209953	June 9, 1998
10	DNA57710-1451	203048	July 1, 1998
	DNA57827-1493	203045	July 1, 1998
	DNA57844-1410	203010	June 23, 1998
	DNA58723-1588	203133	August 18, 1998
	DNA58727-1474	203171	September 1, 1998
15	DNA58730-1607	203221	September 15, 1998
	DNA58732-1650	203290	September 29, 1998
	DNA58737-1473	203136	August 18, 1998
	DNA58743-1609	203154	August 25, 1998
	DNA58747-1384	209868	May 14, 1998
20	DNA58828-1519	203172	September 1, 1998
	DNA58846-1409	209957	June 9, 1998
	DNA58848-1472	209955	June 9, 1998
	DNA58849-1494	209958	June 9, 1998
	DNA58850-1495	209956	June 9, 1998
25	DNA58852-1637	203271	September 22, 1998
	DNA58853-1423	203016	June 23, 1998
	DNA58855-1422	203018	June 23, 1998
	DNA59211-1450	209960	June 9, 1998
	DNA59212-1627	203245	September 9, 1998
30	DNA59213-1487	209959	June 9, 1998
	DNA59219-1613	203220	September 15, 1998
	DNA59497-1496	209941	June 4, 1998
	DNA59602-1436	203051	July 1, 1998
	DNA59603-1419	209944	June 9, 1998
35	DNA59605-1418	203005	June 23, 1998
	DNA59607-1497	209946	June 9, 1998
	DNA59610-1556	209990	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA59612-1466	209947	June 9, 1998
	DNA59613-1417	203007	June 23, 1998
	DNA59616-1465	209991	June 16, 1998
5	DNA59619-1464	203041	July 1, 1998
	DNA59625-1498	209992	June 16, 1998
	DNA59817-1703	203470	November 17, 1998
	DNA59827-1426	203089	August 4, 1998
	DNA59828-1608	203158	August 25, 1998
10	DNA59837-2545	203658	February 9, 1999
	DNA59844-2542	203650	February 9, 1999
	DNA59853-1505	209985	June 16, 1998
	DNA59854-1459	209974	June 16, 1998
	DNA59855-1485	209987	June 16, 1998
15	DNA60278-1530	203170	September 1, 1998
	DNA60283-1484	203043	July 1, 1998
	DNA60608-1577	203126	August 18, 1998
	DNA60611-1524	203175	September 1, 1998
	DNA60619-1482	209993	June 16, 1998
20	DNA60625-1507	209975	June 16, 1998
	DNA60629-1481	209979	June 16, 1998
	DNA60740-1615	203456	November 3, 1998
	DNA61608-1606	203239	September 9, 1998
	DNA61755-1554	203112	August 11, 1998
25	DNA62809-1531	203237	September 9, 1998
	DNA62812-1594	203248	September 9, 1998
	DNA62813-2544	203655	February 9, 1999
	DNA62845-1684	203361	October 20, 1998
	DNA64849-1604	203468	November 17, 1998
30	DNA64852-1589	203127	August 18, 1998
	DNA64863-1573	203251	September 9, 1998
	DNA64881-1602	203240	September 9, 1998
	DNA64902-1667	203317	October 6, 1998
	DNA64952-1568	203222	September 15, 1998
35	DNA65403-1565	203230	September 15, 1998
	DNA65413-1534	203234	September 15, 1998
	DNA65423-1595	203227	September 15, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA66304-1546	203321	October 6, 1998
	DNA66308-1537	203159	August 25, 1998
	DNA66511-1563	203228	September 15, 1998
5	DNA66512-1564	203218	September 15, 1998
	DNA66519-1535	203236	September 15, 1998
	DNA66521-1583	203225	September 15, 1998
	DNA66658-1584	203229	September 15, 1998
	DNA66660-1585	203279	September 22, 1998
10	DNA66669-1597	203272	September 22, 1998
	DNA66674-1599	203281	September 22, 1998
	DNA68836-1656	203455	November 3, 1998
	DNA68862-2546	203652	February 9, 1999
	DNA68866-1644	203283	September 22, 1998
15	DNA68869-1610	203164	August 25, 1998
	DNA68871-1638	203280	September 22, 1998
	DNA68879-1631	203274	September 22, 1998
	DNA68880-1676	203319	October 6, 1998
	DNA68882-1677	203318	October 6, 1998
20	DNA68883-1691	203535	December 15, 1998
	DNA68885-1678	203311	October 6, 1998
	DNA71180-1655	203403	October 27, 1998
	DNA71184-1634	203266	September 22, 1998
	DNA71213-1659	203401	October 27, 1998
25	DNA71234-1651	203402	October 27, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA71277-1636	203285	September 22, 1998
	DNA71286-1687	203357	October 20, 1998
	DNA71883-1660	203475	November 17, 1998
30	DNA73401-1633	203273	September 22, 1998
	DNA73492-1671	203324	October 6, 1998
	DNA73730-1679	203320	October 6, 1998
	DNA73734-1680	203363	October 20, 1998
	DNA73735-1681	203356	October 20, 1998
35	DNA73742-1662	203316	October 6, 1998
	DNA73746-1654	203411	October 27, 1998
	DNA73760-1672	203314	October 6, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA76393-1664	203323	October 6, 1998
	DNA76398-1699	203474	November 17, 1998
	DNA76399-1700	203472	November 17, 1998
5	DNA76522-2500	203469	November 17, 1998
	DNA76533-1689	203410	October 27, 1998
	DNA77303-2502	203479	November 17, 1998
	DNA77626-1705	203536	December 15, 1998
	DNA77648-1688	203408	October 27, 1998
10	DNA81754-2532	203542	December 15, 1998
	DNA81757-2512	203543	December 15, 1998
	DNA82302-2529	203534	December 15, 1998
	DNA82340-2530	203547	December 22, 1998
	DNA87991-2540	203656	February 9, 1999
15	DNA92238-2539	203602	January 20, 1999
	DNA115291-2681	PTA-202	June 8, 1999
	DNA23336-2861	PTA-1673	April 11, 2000
	DNA30862-1396	209920	June 2, 1998
	DNA30871-1157	209380	October 16, 1997
20	DNA32279-1131	209259	September 16, 1997
	DNA33206-1165	209372	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA47361-1154-2	209431	November 7, 1997
	DNA49631-1328	209806	April 28, 1998
25	DNA52594-1270	209679	March 17, 1998
	DNA55800-1263	209680	March 17, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56965-1356	209842	May 6, 1998
	DNA57037-1444	209903	May 27, 1998
30	DNA57695-1340	203006	June 23, 1998
	DNA57834-1339	209954	June 9, 1998
	DNA57841-1522	203458	November 3, 1998
	DNA58847-1383	209879	May 20, 1998
	DNA59493-1420	203050	July 1, 1998
35	DNA59586-1520	203288	September 29, 1998
	DNA59608-2577	203870	March 23, 1999
	DNA59849-1504	209986	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA60292-1506	203540	December 15, 1998
	DNA62377-1381-1	203552	December 22, 1998
	DNA62880-1513	203097	August 4, 1998
5	DNA66672-1586	203265	September 22, 1998
	DNA67962-1649	203291	September 29, 1998
	DNA69555-2867	PTA-1632	April 4, 2000
	DNA71162-2764	PTA-860	October 19, 1999
	DNA71290-1630	203275	September 22, 1998
10	DNA76401-1683	203360	October 20, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA76788-2526	203551	December 22, 1998
	DNA77623-2524	203546	December 22, 1998
	DNA80136-2503	203541	December 15, 1998
15	DNA83568-2692	PTA-386	July 20, 1999
	DNA84210-2576	203818	March 2, 1999
	DNA86576-2595	203868	March 23, 1999
	DNA87976-2593	203888	March 30, 1999
	DNA92256-2596	203891	March 30, 1999
20	DNA92289-2598	PTA-131	May 25, 1999
	DNA96850-2705	PTA-479	August 3, 1999
	DNA96855-2629	PTA-18	May 4, 1999
	DNA96857-2636	PTA-17	May 4, 1999
	DNA96860-2700	PTA-478	August 3, 1999
25	DNA96861-2844	PTA-1436	March 2, 2000
	DNA96866-2698	PTA-491	August 3, 1999
	DNA96870-2676	PTA-254	June 22, 1999
	DNA96872-2674	PTA-550	August 17, 1999
	DNA96878-2626	PTA-23	May 4, 1999
30	DNA96879-2619	203967	April 27, 1999
	DNA96889-2641	PTA-119	May 25, 1999
	DNA96893-2621	PTA-12	May 4, 1999
	DNA96897-2688	PTA-379	July 20, 1999
	DNA98564-2643	PTA-125	May 25, 1999
35	DNA107443-2718	PTA-490	August 3, 1999
	DNA107786-2723	PTA-474	August 3, 1999
	DNA108682-2712	PTA-486	August 3, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA108684-2761	PTA-653	September 14, 1999
	DNA108701-2749	PTA-554	August 17, 1999
	DNA108720-2717	PTA-511	August 10, 1999
5	DNA108726-2729	PTA-514	August 10, 1999
	DNA108728-2760	PTA-654	September 14, 1999
	DNA108738-2767	PTA-862	October 19, 1999
	DNA108743-2722	PTA-508	August 10, 1999
	DNA108758-2759	PTA-655	September 14, 1999
10	DNA108765-2758	PTA-657	September 14, 1999
	DNA108783-2747	PTA-616	August 31, 1999
	DNA108789-2748	PTA-547	August 17, 1999
	DNA108806-2724	PTA-610	August 31, 1999
	DNA108936-2719	PTA-519	August 10, 1999
15	DNA119510-2771	PTA-947	November 9, 1999
	DNA119517-2778	PTA-951	November 16, 1999
	DNA119535-2756	PTA-613	August 31, 1999
	DNA119537-2777	PTA-956	November 16, 1999
	DNA119714-2851	PTA-1537	March 21, 2000
20	DNA125170-2780	PTA-953	November 16, 1999
	DNA129594-2841	PTA-1481	March 14, 2000
	DNA129793-2857	PTA-1733	April 18, 2000
	DNA130809-2769	PTA-949	November 9, 1999
	DNA131639-2874	PTA-1784	April 25, 2000
25	DNA131649-2855	PTA-1482	March 14, 2000
	DNA131652-2876	PTA-1628	April 4, 2000
	DNA131658-2875	PTA-1671	April 11, 2000
	DNA132162-2770	PTA-950	November 9, 1999
	DNA136110-2763	PTA-652	September 14, 1999
30	DNA139592-2866	PTA-1587	March 28, 2000
	DNA139608-2856	PTA-1581	March 28, 2000
	DNA143292-2848	PTA-1778	April 25, 2000
	DNA144844-2843	PTA-1536	March 21, 2000
	DNA144857-2845	PTA-1589	March 28, 2000
35	DNA145841-2868	PTA-1678	April 11, 2000
	DNA148004-2882	PTA-1779	April 25, 2000
	DNA149893-2873	PTA-1672	April 11, 2000

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA149930-2884	PTA-1668	April 11, 2000
	DNA150157-2898	PTA-1777	April 25, 2000
	DNA150163-2842	PTA-1533	March 21, 2000
5	DNA153579-2894	PTA-1729	April 18, 2000
	DNA164625-2890	PTA-1535	March 21, 2000
	DNA57838-1337	203014	June 23, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA66675-1587	203282	September 22, 1998
10	DNA76532-1702	203473	November 17, 1998
	DNA105849-2704	PTA-473	August 3, 1999
	DNA83500-2506	203391	October 29, 1998

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

30 EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

35 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH

6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

5 **EXAMPLE 6: Expression of PRO in *E. coli***

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify

expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

E. coli paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., *supra*. The resulting vector is called pRK5-

PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ^{35}S -cysteine and 200 μ Ci/ml ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompariyac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be

concentrated and purified by any selected method, such as by Ni²⁺-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Qiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3 x 10⁷ cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μ m filtered PS20 with 5% 0.2 μ m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3 x 10⁵ cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2 x 10⁶ cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μ m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional

equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then

digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al.,

5 Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated
10 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded
15 onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed
20 against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

25 EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled
30 artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional
35 immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 12: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO

polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, *J. Biochem.*, 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- α Release In Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay:

PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

EXAMPLE 15: Promotion of Chondrocyte Redifferentiation (Assay 129)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage

disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 22 µl of media containing 100 µg/ml Hoechst 33342 and 50 µg/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the > 50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

PRO6029 polypeptide tested positive in this assay.

EXAMPLE 16: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was

prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

Table 8

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
20	PRO276	lung tumor	universal normal control
	PRO284	colon tumor	universal normal control
	PRO284	lung tumor	universal normal control
	PRO284	breast tumor	universal normal control
	PRO193	colon tumor	universal normal control
	PRO193	lung tumor	universal normal control
25	PRO193	breast tumor	universal normal control
	PRO193	prostate tumor	universal normal control
	PRO190	colon tumor	universal normal control
	PRO190	lung tumor	universal normal control
	PRO190	breast tumor	universal normal control
30	PRO180	colon tumor	universal normal control
	PRO180	lung tumor	universal normal control
	PRO180	breast tumor	universal normal control
	PRO194	colon tumor	universal normal control
	PRO194	lung tumor	universal normal control
35	PRO194	breast tumor	universal normal control
	PRO194	cervical tumor	universal normal control
	PRO218	colon tumor	universal normal control
	PRO218	lung tumor	universal normal control
40	PRO260	colon tumor	universal normal control
	PRO260	lung tumor	universal normal control
	PRO260	breast tumor	universal normal control
	PRO260	rectal tumor	universal normal control
	PRO233	colon tumor	universal normal control
	PRO233	lung tumor	universal normal control
45	PRO233	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO234	colon tumor	universal normal control
	PRO234	lung tumor	universal normal control
5	PRO234	breast tumor	universal normal control
	PRO234	liver tumor	universal normal control
	PRO236	colon tumor	universal normal control
	PRO236	lung tumor	universal normal control
	PRO236	breast tumor	universal normal control
	PRO244	colon tumor	universal normal control
10	PRO244	lung tumor	universal normal control
	PRO262	colon tumor	universal normal control
	PRO262	lung tumor	universal normal control
	PRO262	breast tumor	universal normal control
	PRO271	colon tumor	universal normal control
15	PRO271	lung tumor	universal normal control
	PRO268	colon tumor	universal normal control
	PRO268	lung tumor	universal normal control
	PRO268	breast tumor	universal normal control
	PRO270	colon tumor	universal normal control
20	PRO270	lung tumor	universal normal control
	PRO270	breast tumor	universal normal control
	PRO270	liver tumor	universal normal control
	PRO355	lung tumor	universal normal control
	PRO355	breast tumor	universal normal control
25	PRO355	prostate tumor	universal normal control
	PRO298	colon tumor	universal normal control
	PRO298	lung tumor	universal normal control
	PRO298	breast tumor	universal normal control
	PRO299	colon tumor	universal normal control
30	PRO299	lung tumor	universal normal control
	PRO299	breast tumor	universal normal control
	PRO296	colon tumor	universal normal control
	PRO296	breast tumor	universal normal control
	PRO329	colon tumor	universal normal control
35	PRO329	lung tumor	universal normal control
	PRO329	breast tumor	universal normal control
	PRO330	colon tumor	universal normal control
	PRO330	lung tumor	universal normal control
	PRO294	lung tumor	universal normal control
40	PRO294	breast tumor	universal normal control
	PRO300	colon tumor	universal normal control
	PRO300	lung tumor	universal normal control
	PRO300	breast tumor	universal normal control
	PRO307	lung tumor	universal normal control
45	PRO334	colon tumor	universal normal control
	PRO334	lung tumor	universal normal control
	PRO334	breast tumor	universal normal control
	PRO334	prostate tumor	universal normal control
	PRO352	colon tumor	universal normal control
50	PRO352	lung tumor	universal normal control
	PRO352	breast tumor	universal normal control
	PRO352	liver tumor	universal normal control
	PRO710	breast tumor	universal normal control
	PRO873	colon tumor	universal normal control
55	PRO873	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO873	breast tumor	universal normal control
	PRO873	prostate tumor	universal normal control
5	PRO354	colon tumor	universal normal control
	PRO354	lung tumor	universal normal control
	PRO354	breast tumor	universal normal control
	PRO1151	lung tumor	universal normal control
	PRO1151	breast tumor	universal normal control
10	PRO382	colon tumor	universal normal control
	PRO382	lung tumor	universal normal control
	PRO382	breast tumor	universal normal control
	PRO1864	lung tumor	universal normal control
	PRO1864	breast tumor	universal normal control
	PRO1864	liver tumor	universal normal control
15	PRO386	colon tumor	universal normal control
	PRO386	lung tumor	universal normal control
	PRO386	prostate tumor	universal normal control
	PRO541	colon tumor	universal normal control
	PRO541	lung tumor	universal normal control
20	PRO541	breast tumor	universal normal control
	PRO852	breast tumor	universal normal control
	PRO700	colon tumor	universal normal control
	PRO700	lung tumor	universal normal control
	PRO700	breast tumor	universal normal control
25	PRO700	rectal tumor	universal normal control
	PRO708	colon tumor	universal normal control
	PRO708	lung tumor	universal normal control
	PRO708	breast tumor	universal normal control
	PRO707	colon tumor	universal normal control
30	PRO707	lung tumor	universal normal control
	PRO864	colon tumor	universal normal control
	PRO864	lung tumor	universal normal control
	PRO864	breast tumor	universal normal control
35	PRO706	colon tumor	universal normal control
	PRO706	lung tumor	universal normal control
	PRO706	breast tumor	universal normal control
	PRO706	liver tumor	universal normal control
	PRO732	lung tumor	universal normal control
	PRO732	breast tumor	universal normal control
40	PRO732	cervical tumor	universal normal control
	PRO537	colon tumor	universal normal control
	PRO537	lung tumor	universal normal control
	PRO537	breast tumor	universal normal control
45	PRO545	lung tumor	universal normal control
	PRO545	breast tumor	universal normal control
	PRO718	lung tumor	universal normal control
	PRO718	breast tumor	universal normal control
	PRO872	lung tumor	universal normal control
	PRO872	breast tumor	universal normal control
50	PRO872	liver tumor	universal normal control
	PRO704	colon tumor	universal normal control
	PRO704	lung tumor	universal normal control
	PRO704	breast tumor	universal normal control
	PRO705	lung tumor	universal normal control
55	PRO705	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO871	lung tumor	universal normal control
	PRO871	breast tumor	universal normal control
	PRO871	liver tumor	universal normal control
5	PRO702	lung tumor	universal normal control
	PRO944	colon tumor	universal normal control
	PRO944	lung tumor	universal normal control
	PRO944	rectal tumor	universal normal control
	PRO739	lung tumor	universal normal control
10	PRO739	breast tumor	universal normal control
	PRO739	prostate tumor	universal normal control
	PRO941	colon tumor	universal normal control
	PRO941	lung tumor	universal normal control
	PRO941	breast tumor	universal normal control
15	PRO941	rectal tumor	universal normal control
	PRO1082	lung tumor	universal normal control
	PRO1082	breast tumor	universal normal control
	PRO1133	colon tumor	universal normal control
	PRO1133	lung tumor	universal normal control
20	PRO983	colon tumor	universal normal control
	PRO983	lung tumor	universal normal control
	PRO983	breast tumor	universal normal control
	PRO784	colon tumor	universal normal control
	PRO784	lung tumor	universal normal control
25	PRO784	breast tumor	universal normal control
	PRO784	prostate tumor	universal normal control
	PRO783	colon tumor	universal normal control
	PRO783	lung tumor	universal normal control
	PRO783	breast tumor	universal normal control
30	PRO783	liver tumor	universal normal control
	PRO940	colon tumor	universal normal control
	PRO940	lung tumor	universal normal control
	PRO940	breast tumor	universal normal control
	PRO768	colon tumor	universal normal control
35	PRO768	lung tumor	universal normal control
	PRO768	breast tumor	universal normal control
	PRO1079	colon tumor	universal normal control
	PRO1079	lung tumor	universal normal control
	PRO1079	breast tumor	universal normal control
40	PRO1079	rectal tumor	universal normal control
	PRO1078	colon tumor	universal normal control
	PRO1078	lung tumor	universal normal control
	PRO1018	colon tumor	universal normal control
	PRO1018	lung tumor	universal normal control
45	PRO1018	breast tumor	universal normal control
	PRO793	colon tumor	universal normal control
	PRO793	lung tumor	universal normal control
	PRO793	breast tumor	universal normal control
	PRO793	rectal tumor	universal normal control
50	PRO1773	colon tumor	universal normal control
	PRO1773	lung tumor	universal normal control
	PRO1773	prostate tumor	universal normal control
	PRO1014	lung tumor	universal normal control
	PRO1014	breast tumor	universal normal control
55	PRO1013	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1013	lung tumor	universal normal control
	PRO1013	breast tumor	universal normal control
	PRO1013	liver tumor	universal normal control
5	PRO937	colon tumor	universal normal control
	PRO937	lung tumor	universal normal control
	PRO937	breast tumor	universal normal control
	PRO937	cervical tumor	universal normal control
	PRO937	rectal tumor	universal normal control
10	PRO1477	lung tumor	universal normal control
	PRO1477	breast tumor	universal normal control
	PRO1477	rectal tumor	universal normal control
	PRO842	colon tumor	universal normal control
	PRO842	lung tumor	universal normal control
15	PRO842	breast tumor	universal normal control
	PRO839	colon tumor	universal normal control
	PRO1180	colon tumor	universal normal control
	PRO1180	lung tumor	universal normal control
	PRO1180	liver tumor	universal normal control
20	PRO1134	lung tumor	universal normal control
	PRO1134	breast tumor	universal normal control
	PRO1134	prostate tumor	universal normal control
	PRO1115	colon tumor	universal normal control
	PRO1115	lung tumor	universal normal control
25	PRO1115	breast tumor	universal normal control
	PRO1277	colon tumor	universal normal control
	PRO1277	lung tumor	universal normal control
	PRO1135	lung tumor	universal normal control
	PRO1135	breast tumor	universal normal control
30	PRO1135	cervical tumor	universal normal control
	PRO827	colon tumor	universal normal control
	PRO827	lung tumor	universal normal control
	PRO827	prostate tumor	universal normal control
	PRO827	cervical tumor	universal normal control
35	PRO1057	lung tumor	universal normal control
	PRO1057	breast tumor	universal normal control
	PRO1113	colon tumor	universal normal control
	PRO1113	lung tumor	universal normal control
	PRO1006	colon tumor	universal normal control
40	PRO1006	lung tumor	universal normal control
	PRO1006	breast tumor	universal normal control
	PRO1006	rectal tumor	universal normal control
	PRO1074	lung tumor	universal normal control
	PRO1074	rectal tumor	universal normal control
45	PRO1073	lung tumor	universal normal control
	PRO1073	breast tumor	universal normal control
	PRO1136	colon tumor	universal normal control
	PRO1136	lung tumor	universal normal control
	PRO1136	breast tumor	universal normal control
50	PRO1004	lung tumor	universal normal control
	PRO1344	colon tumor	universal normal control
	PRO1344	lung tumor	universal normal control
	PRO1344	breast tumor	universal normal control
	PRO1344	rectal tumor	universal normal control
55	PRO1110	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1110	lung tumor	universal normal control
	PRO1110	breast tumor	universal normal control
5	PRO1378	colon tumor	universal normal control
	PRO1378	lung tumor	universal normal control
	PRO1378	prostate tumor	universal normal control
	PRO1378	cervical tumor	universal normal control
	PRO1481	colon tumor	universal normal control
	PRO1481	lung tumor	universal normal control
10	PRO1109	lung tumor	universal normal control
	PRO1109	breast tumor	universal normal control
	PRO1383	colon tumor	universal normal control
	PRO1383	lung tumor	universal normal control
	PRO1383	breast tumor	universal normal control
15	PRO1072	lung tumor	universal normal control
	PRO1189	colon tumor	universal normal control
	PRO1189	lung tumor	universal normal control
	PRO1189	breast tumor	universal normal control
	PRO1189	prostate tumor	universal normal control
20	PRO1003	colon tumor	universal normal control
	PRO1003	lung tumor	universal normal control
	PRO1003	breast tumor	universal normal control
	PRO1003	liver tumor	universal normal control
	PRO1003	rectal tumor	universal normal control
25	PRO1108	colon tumor	universal normal control
	PRO1108	lung tumor	universal normal control
	PRO1108	breast tumor	universal normal control
	PRO1137	colon tumor	universal normal control
	PRO1137	lung tumor	universal normal control
30	PRO1137	breast tumor	universal normal control
	PRO1138	colon tumor	universal normal control
	PRO1138	lung tumor	universal normal control
	PRO1138	breast tumor	universal normal control
35	PRO1415	colon tumor	universal normal control
	PRO1415	lung tumor	universal normal control
	PRO1415	prostate tumor	universal normal control
	PRO1054	lung tumor	universal normal control
	PRO1054	breast tumor	universal normal control
40	PRO994	colon tumor	universal normal control
	PRO994	lung tumor	universal normal control
	PRO994	rectal tumor	universal normal control
	PRO1069	lung tumor	universal normal control
	PRO1069	breast tumor	universal normal control
45	PRO1411	colon tumor	universal normal control
	PRO1411	lung tumor	universal normal control
	PRO1129	lung tumor	universal normal control
	PRO1129	rectal tumor	universal normal control
	PRO1359	colon tumor	universal normal control
	PRO1359	lung tumor	universal normal control
50	PRO1359	breast tumor	universal normal control
	PRO1359	prostate tumor	universal normal control
	PRO1139	lung tumor	universal normal control
	PRO1065	lung tumor	universal normal control
	PRO1028	colon tumor	universal normal control
55	PRO1028	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1028	breast tumor	universal normal control
	PRO1028	cervical tumor	universal normal control
5	PRO1027	colon tumor	universal normal control
	PRO1027	lung tumor	universal normal control
	PRO1027	breast tumor	universal normal control
	PRO1140	colon tumor	universal normal control
	PRO1140	breast tumor	universal normal control
10	PRO1291	colon tumor	universal normal control
	PRO1291	breast tumor	universal normal control
	PRO1105	colon tumor	universal normal control
	PRO1105	lung tumor	universal normal control
	PRO1026	lung tumor	universal normal control
	PRO1026	prostate tumor	universal normal control
15	PRO1104	colon tumor	universal normal control
	PRO1104	lung tumor	universal normal control
	PRO1104	breast tumor	universal normal control
	PRO1100	colon tumor	universal normal control
	PRO1100	lung tumor	universal normal control
20	PRO1100	breast tumor	universal normal control
	PRO1100	rectal tumor	universal normal control
	PRO1141	lung tumor	universal normal control
	PRO1772	colon tumor	universal normal control
	PRO1772	lung tumor	universal normal control
25	PRO1772	breast tumor	universal normal control
	PRO1772	cervical tumor	universal normal control
	PRO1064	colon tumor	universal normal control
	PRO1064	lung tumor	universal normal control
	PRO1379	colon tumor	universal normal control
30	PRO1379	lung tumor	universal normal control
	PRO1379	cervical tumor	universal normal control
	PRO3573	lung tumor	universal normal control
	PRO3573	breast tumor	universal normal control
	PRO3566	colon tumor	universal normal control
35	PRO3566	lung tumor	universal normal control
	PRO1156	lung tumor	universal normal control
	PRO1156	breast tumor	universal normal control
	PRO1156	prostate tumor	universal normal control
	PRO1098	colon tumor	universal normal control
40	PRO1098	lung tumor	universal normal control
	PRO1098	rectal tumor	universal normal control
	PRO1128	colon tumor	universal normal control
	PRO1128	lung tumor	universal normal control
	PRO1128	breast tumor	universal normal control
45	PRO1248	lung tumor	universal normal control
	PRO1248	breast tumor	universal normal control
	PRO1127	colon tumor	universal normal control
	PRO1127	lung tumor	universal normal control
	PRO1127	breast tumor	universal normal control
50	PRO1316	colon tumor	universal normal control
	PRO1316	lung tumor	universal normal control
	PRO1316	breast tumor	universal normal control
	PRO1197	colon tumor	universal normal control
	PRO1197	lung tumor	universal normal control
55	PRO1197	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1125	lung tumor	universal normal control
	PRO1158	breast tumor	universal normal control
5	PRO1124	colon tumor	universal normal control
	PRO1124	lung tumor	universal normal control
	PRO1380	colon tumor	universal normal control
	PRO1380	lung tumor	universal normal control
	PRO1380	breast tumor	universal normal control
	PRO1380	liver tumor	universal normal control
10	PRO1377	colon tumor	universal normal control
	PRO1377	lung tumor	universal normal control
	PRO1287	lung tumor	universal normal control
	PRO1287	breast tumor	universal normal control
15	PRO1249	lung tumor	universal normal control
	PRO1249	breast tumor	universal normal control
	PRO1335	colon tumor	universal normal control
	PRO1335	lung tumor	universal normal control
	PRO1335	breast tumor	universal normal control
	PRO3572	lung tumor	universal normal control
20	PRO1599	colon tumor	universal normal control
	PRO1599	lung tumor	universal normal control
	PRO1599	breast tumor	universal normal control
	PRO1374	lung tumor	universal normal control
	PRO1374	breast tumor	universal normal control
25	PRO1345	lung tumor	universal normal control
	PRO1345	breast tumor	universal normal control
	PRO1311	lung tumor	universal normal control
	PRO1311	breast tumor	universal normal control
	PRO1357	colon tumor	universal normal control
30	PRO1357	lung tumor	universal normal control
	PRO1557	colon tumor	universal normal control
	PRO1557	lung tumor	universal normal control
	PRO1557	breast tumor	universal normal control
35	PRO1305	colon tumor	universal normal control
	PRO1305	lung tumor	universal normal control
	PRO1305	breast tumor	universal normal control
	PRO1302	colon tumor	universal normal control
	PRO1302	lung tumor	universal normal control
	PRO1302	breast tumor	universal normal control
40	PRO1302	rectal tumor	universal normal control
	PRO1266	colon tumor	universal normal control
	PRO1336	colon tumor	universal normal control
	PRO1336	lung tumor	universal normal control
	PRO1336	breast tumor	universal normal control
45	PRO1278	colon tumor	universal normal control
	PRO1278	lung tumor	universal normal control
	PRO1270	breast tumor	universal normal control
	PRO1298	colon tumor	universal normal control
	PRO1298	lung tumor	universal normal control
50	PRO1301	lung tumor	universal normal control
	PRO1301	breast tumor	universal normal control
	PRO1268	colon tumor	universal normal control
	PRO1268	breast tumor	universal normal control
55	PRO1327	lung tumor	universal normal control
	PRO1327	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1328	colon tumor	universal normal control
	PRO1328	lung tumor	universal normal control
	PRO1328	breast tumor	universal normal control
5	PRO1329	colon tumor	universal normal control
	PRO1329	lung tumor	universal normal control
	PRO1329	breast tumor	universal normal control
	PRO1339	colon tumor	universal normal control
	PRO1339	lung tumor	universal normal control
10	PRO1342	colon tumor	universal normal control
	PRO1342	lung tumor	universal normal control
	PRO1342	breast tumor	universal normal control
	PRO1342	rectal tumor	universal normal control
	PRO1487	colon tumor	universal normal control
15	PRO1487	breast tumor	universal normal control
	PRO3579	lung tumor	universal normal control
	PRO3579	breast tumor	universal normal control
	PRO1472	colon tumor	universal normal control
	PRO1472	lung tumor	universal normal control
20	PRO1385	lung tumor	universal normal control
	PRO1385	breast tumor	universal normal control
	PRO1461	colon tumor	universal normal control
	PRO1461	lung tumor	universal normal control
	PRO1461	breast tumor	universal normal control
25	PRO1429	colon tumor	universal normal control
	PRO1429	lung tumor	universal normal control
	PRO1429	breast tumor	universal normal control
	PRO1568	lung tumor	universal normal control
	PRO1568	breast tumor	universal normal control
30	PRO1569	colon tumor	universal normal control
	PRO1569	lung tumor	universal normal control
	PRO1569	breast tumor	universal normal control
	PRO1753	colon tumor	universal normal control
	PRO1753	lung tumor	universal normal control
35	PRO1570	colon tumor	universal normal control
	PRO1570	lung tumor	universal normal control
	PRO1570	breast tumor	universal normal control
	PRO1570	prostate tumor	universal normal control
	PRO1570	rectal tumor	universal normal control
40	PRO1559	colon tumor	universal normal control
	PRO1559	lung tumor	universal normal control
	PRO1559	breast tumor	universal normal control
	PRO1486	lung tumor	universal normal control
	PRO1486	breast tumor	universal normal control
45	PRO1433	colon tumor	universal normal control
	PRO1433	lung tumor	universal normal control
	PRO1433	breast tumor	universal normal control
	PRO1433	rectal tumor	universal normal control
	PRO1490	lung tumor	universal normal control
50	PRO1490	breast tumor	universal normal control
	PRO1482	lung tumor	universal normal control
	PRO1482	breast tumor	universal normal control
	PRO1409	colon tumor	universal normal control
	PRO1409	lung tumor	universal normal control
55	PRO1409	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1446	colon tumor	universal normal control
	PRO1446	lung tumor	universal normal control
5	PRO1446	breast tumor	universal normal control
	PRO1446	prostate tumor	universal normal control
	PRO1604	colon tumor	universal normal control
	PRO1604	lung tumor	universal normal control
	PRO1604	breast tumor	universal normal control
10	PRO1491	colon tumor	universal normal control
	PRO1491	lung tumor	universal normal control
	PRO1491	breast tumor	universal normal control
	PRO1431	colon tumor	universal normal control
	PRO1431	lung tumor	universal normal control
15	PRO1563	colon tumor	universal normal control
	PRO1563	lung tumor	universal normal control
	PRO1563	breast tumor	universal normal control
	PRO1571	colon tumor	universal normal control
	PRO1571	lung tumor	universal normal control
	PRO1571	breast tumor	universal normal control
20	PRO1572	lung tumor	universal normal control
	PRO1572	prostate tumor	universal normal control
	PRO1573	lung tumor	universal normal control
	PRO1573	breast tumor	universal normal control
25	PRO1508	lung tumor	universal normal control
	PRO1508	breast tumor	universal normal control
	PRO1485	colon tumor	universal normal control
	PRO1485	lung tumor	universal normal control
	PRO1564	colon tumor	universal normal control
	PRO1564	lung tumor	universal normal control
30	PRO1564	breast tumor	universal normal control
	PRO1550	colon tumor	universal normal control
	PRO1550	lung tumor	universal normal control
	PRO1550	breast tumor	universal normal control
35	PRO1757	lung tumor	universal normal control
	PRO1757	breast tumor	universal normal control
	PRO1757	prostate tumor	universal normal control
	PRO1758	lung tumor	universal normal control
	PRO1781	colon tumor	universal normal control
	PRO1781	lung tumor	universal normal control
40	PRO1781	breast tumor	universal normal control
	PRO1606	lung tumor	universal normal control
	PRO1606	breast tumor	universal normal control
	PRO1784	colon tumor	universal normal control
	PRO1784	lung tumor	universal normal control
45	PRO1784	breast tumor	universal normal control
	PRO1774	colon tumor	universal normal control
	PRO1774	lung tumor	universal normal control
	PRO1774	breast tumor	universal normal control
50	PRO1605	colon tumor	universal normal control
	PRO1605	lung tumor	universal normal control
	PRO1605	prostate tumor	universal normal control
	PRO1928	colon tumor	universal normal control
	PRO1928	lung tumor	universal normal control
	PRO1928	cervical tumor	universal normal control
55	PRO1865	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1865	liver tumor	universal normal control
	PRO1925	lung tumor	universal normal control
	PRO1926	liver tumor	universal normal control
5	PRO2630	colon tumor	universal normal control
	PRO2630	lung tumor	universal normal control
	PRO2630	breast tumor	universal normal control
	PRO2630	liver tumor	universal normal control
	PRO3443	colon tumor	universal normal control
10	PRO3443	lung tumor	universal normal control
	PRO3443	breast tumor	universal normal control
	PRO3301	colon tumor	universal normal control
	PRO3301	lung tumor	universal normal control
	PRO3301	breast tumor	universal normal control
15	PRO3301	rectal tumor	universal normal control
	PRO3442	colon tumor	universal normal control
	PRO3442	lung tumor	universal normal control
	PRO3442	rectal tumor	universal normal control
	PRO4978	colon tumor	universal normal control
20	PRO4978	lung tumor	universal normal control
	PRO4978	breast tumor	universal normal control
	PRO4978	rectal tumor	universal normal control
	PRO5801	colon tumor	universal normal control
	PRO5801	breast tumor	universal normal control
25	PRO19630	colon tumor	universal normal control
	PRO203	colon tumor	universal normal control
	PRO204	colon tumor	universal normal control
	PRO204	lung tumor	universal normal control
	PRO204	breast tumor	universal normal control
30	PRO204	prostate tumor	universal normal control
	PRO210	colon tumor	universal normal control
	PRO210	lung tumor	universal normal control
	PRO223	lung tumor	universal normal control
	PRO223	breast tumor	universal normal control
35	PRO247	colon tumor	universal normal control
	PRO247	lung tumor	universal normal control
	PRO247	breast	universal normal control
	PRO358	lung tumor	universal normal control
	PRO358	breast tumor	universal normal control
40	PRO358	prostate tumor	universal normal control
	PRO724	lung tumor	universal normal control
	PRO868	colon tumor	universal normal control
	PRO868	lung tumor	universal normal control
	PRO868	prostate tumor	universal normal control
45	PRO868	rectal tumor	universal normal control
	PRO740	colon tumor	universal normal control
	PRO1478	colon tumor	universal normal control
	PRO1478	lung tumor	universal normal control
	PRO162	colon tumor	universal normal control
50	PRO162	lung tumor	universal normal control
	PRO162	breast tumor	universal normal control
	PRO828	colon tumor	universal normal control
	PRO828	lung tumor	universal normal control
	PRO828	breast tumor	universal normal control
55	PRO828	cervical tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO828	liver tumor	universal normal control
	PRO819	lung tumor	universal normal control
5	PRO819	breast tumor	universal normal control
	PRO819	rectal tumor	universal normal control
	PRO813	colon tumor	universal normal control
	PRO813	lung tumor	universal normal control
	PRO813	breast tumor	universal normal control
	PRO813	prostate tumor	universal normal control
10	PRO1194	colon tumor	universal normal control
	PRO1194	lung tumor	universal normal control
	PRO1194	breast tumor	universal normal control
	PRO887	colon tumor	universal normal control
	PRO887	lung tumor	universal normal control
15	PRO887	rectal tumor	universal normal control
	PRO1071	colon tumor	universal normal control
	PRO1071	lung tumor	universal normal control
	PRO1071	breast tumor	universal normal control
	PRO1029	colon tumor	universal normal control
20	PRO1029	lung tumor	universal normal control
	PRO1029	breast tumor	universal normal control
	PRO1190	lung tumor	universal normal control
	PRO1190	breast tumor	universal normal control
	PRO4334	lung tumor	universal normal control
25	PRO1155	colon tumor	universal normal control
	PRO1155	lung tumor	universal normal control
	PRO1157	breast tumor	universal normal control
	PRO1157	cervical tumor	universal normal control
	PRO1122	lung tumor	universal normal control
30	PRO1122	breast tumor	universal normal control
	PRO1183	colon tumor	universal normal control
	PRO1183	lung tumor	universal normal control
	PRO1183	breast tumor	universal normal control
	PRO1337	colon tumor	universal normal control
35	PRO1337	lung tumor	universal normal control
	PRO1337	breast tumor	universal normal control
	PRO1480	colon tumor	universal normal control
	PRO1480	lung tumor	universal normal control
	PRO1480	breast tumor	universal normal control
40	PRO19645	colon tumor	universal normal control
	PRO9782	colon tumor	universal normal control
	PRO1419	colon tumor	universal normal control
	PRO1575	colon tumor	universal normal control
	PRO1575	lung tumor	universal normal control
45	PRO1567	colon tumor	universal normal control
	PRO1567	lung tumor	universal normal control
	PRO1567	breast tumor	universal normal control
	PRO1891	colon tumor	universal normal control
	PRO1889	colon tumor	universal normal control
50	PRO1889	lung tumor	universal normal control
	PRO1785	lung tumor	universal normal control
	PRO1785	prostate tumor	universal normal control
	PRO6003	colon tumor	universal normal control
	PRO4333	colon tumor	universal normal control
55	PRO4356	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4352	colon tumor	universal normal control
	PRO4354	colon tumor	universal normal control
	PRO4354	lung tumor	universal normal control
5	PRO4354	prostate tumor	universal normal control
	PRO4369	colon tumor	universal normal control
	PRO6030	colon tumor	universal normal control
	PRO4433	colon tumor	universal normal control
	PRO4424	colon tumor	universal normal control
10	PRO4424	breast tumor	universal normal control
	PRO6017	colon tumor	universal normal control
	PRO19563	colon tumor	universal normal control
	PRO6015	colon tumor	universal normal control
	PRO5779	colon tumor	universal normal control
15	PRO5776	colon tumor	universal normal control
	PRO4430	lung tumor	universal normal control
	PRO4421	colon tumor	universal normal control
	PRO4499	colon tumor	universal normal control
	PRO4423	colon tumor	universal normal control
20	PRO5998	colon tumor	universal normal control
	PRO5998	lung tumor	universal normal control
	PRO4501	colon tumor	universal normal control
	PRO6240	colon tumor	universal normal control
	PRO6245	colon tumor	universal normal control
25	PRO6175	colon tumor	universal normal control
	PRO9742	colon tumor	universal normal control
	PRO7179	colon tumor	universal normal control
	PRO6239	colon tumor	universal normal control
	PRO6493	colon tumor	universal normal control
30	PRO9741	colon tumor	universal normal control
	PRO9822	colon tumor	universal normal control
	PRO6244	colon tumor	universal normal control
	PRO9740	colon tumor	universal normal control
	PRO9739	colon tumor	universal normal control
35	PRO7177	colon tumor	universal normal control
	PRO7178	colon tumor	universal normal control
	PRO6246	colon tumor	universal normal control
	PRO6241	colon tumor	universal normal control
	PRO9835	colon tumor	universal normal control
40	PRO9857	colon tumor	universal normal control
	PRO7436	colon tumor	universal normal control
	PRO9856	colon tumor	universal normal control
	PRO19605	colon tumor	universal normal control
	PRO9859	colon tumor	universal normal control
45	PRO12970	colon tumor	universal normal control
	PRO19626	colon tumor	universal normal control
	PRO9883	colon tumor	universal normal control
	PRO19670	colon tumor	universal normal control
	PRO19624	colon tumor	universal normal control
50	PRO19680	colon tumor	universal normal control
	PRO19675	colon tumor	universal normal control
	PRO9834	colon tumor	universal normal control
	PRO9744	colon tumor	universal normal control
	PRO19644	colon tumor	universal normal control
55	PRO19625	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO19597	colon tumor	universal normal control
	PRO16090	colon tumor	universal normal control
	PRO19576	colon tumor	universal normal control
5	PRO19646	colon tumor	universal normal control
	PRO19814	colon tumor	universal normal control
	PRO19669	colon tumor	universal normal control
	PRO19818	colon tumor	universal normal control
	PRO20088	colon tumor	universal normal control
10	PRO16089	colon tumor	universal normal control
	PRO20025	colon tumor	universal normal control
	PRO20040	colon tumor	universal normal control
	PRO1760	adrenal tumor	universal normal control
	PRO1760	breast tumor	universal normal control
15	PRO1760	cervical tumor	universal normal control
	PRO1760	colon tumor	universal normal control
	PRO1760	liver tumor	universal normal control
	PRO1760	lung tumor	universal normal control
	PRO1760	prostate tumor	universal normal control
20	PRO1760	rectal tumor	universal normal control
	PRO6029	adrenal tumor	universal normal control
	PRO6029	colon tumor	universal normal control
	PRO6029	prostate tumor	universal normal control
	PRO1801	colon tumor	universal normal control
25	PRO1801	lung tumor	universal normal control

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID

[illegible]

NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID

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4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.
5. A vector comprising the nucleic acid of Claim 1.
6. A host cell comprising the vector of Claim 5.
7. The host cell of Claim 6, wherein said cell is a CHO cell.
8. The host cell of Claim 6, wherein said cell is an *E. coli*.
9. The host cell of Claim 6, wherein said cell is a yeast cell.
10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID

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NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Pc region of an immunoglobulin.

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16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

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18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure

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188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure

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(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ

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- NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), with its associated signal peptide; or
- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18

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- 10 19. An isolated polypeptide having at least 80% amino acid sequence identity to:
- (a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194),

NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID

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(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

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306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID
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(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure

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NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure

[illegible]

572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

20. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- α from said blood is stimulated.

10

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

15

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

20

23. The method of Claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

25

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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FIGURE 1

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCCGCCCTCTCCGCCTTCTGCATCGCGGCTTCGGCG
GCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCGTGAGGGGGTCGGCACGGGGAGTCGGGCGGCTCT
TGTGCATCTTGGCTACCTGTGGGTGGAAGATGTCGGACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGC
GCTATTGGTTTCGCCGCCACCGTCGCCGTGCCCTTGGTCGGCAAACCTCGGCCTCATCAGCCCCGGCTACCTCTTCC
TCTGGCCCCGAAGCCTTCCCTTTATCGCTTTTCTAGATTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGGTC
CAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGACTTGAACAGGAGCTT
TTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTGGATTTCATCGTGATTACTGGCTTAGCAA
TGGATATGCAGTTGCTGATGATTCTCTGATCATGTGAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGA
TTGTATCATTTTGGTTTGGAAACAGATTTAAGGCCTGCTATTTACCCTGGGTTATCCTTGGATTCAACTATATCA
TCGGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTCCTAATGTTTCTAGATACC
CAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGGCTGCCAGTAGGAGAGGAG
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGGAGGCGGGAGACACA
ACTGGGGCCAGGGCTTTCGACTTGGAGACCAGTGAAGGGGCGGCTCGGGCAGCCGCTCCTCTCAAGCCACATTT
CCTCCCAGTGCTGGGTGCACCTAACAACTGCCCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCCACAGTTTTCACGATTTCTATTCA
AGTCCTTACTGCTGTGAAGAACAATACCACTGTGCAAATTGCAAACTGACTACATTTTTTGGTGTCTTCTCT
TCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTTAATCTGCTGGCATTGAGCTGGGCTGGGTACCAA
ACCCTTCCCAAAAGGACCTTATCTCTTTCTTGACACATGCTCTCTCCACTTTTCCCAACCCCCACATTTGCA
ACTAGAAAAAGTTGCCATAAAATGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAAGGCTGGT
CACAACTCATATTACGTTATTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAGAGAGCCACG
GATGAAGCGTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTTAACCGTTTGGCACTCTTCAGATATT
TTTTATAAAAAAGTACCAGTGAATCATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGGTTGGTCTGG
GTGTTTGTCTTCTGAGCTAAGTGATCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGG
GGATGCACCCCTTTGCGTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCCATTTCAATC
TCATTCGGATATGTGTTTCATTGAGTAAAGGAGGAGAGACCCTCATACGCTATTTAAATGTCACTTTTTTGCCTA
TCCCCCGTTTTTTGGTCATGTTTCAATTAATTGTGAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTA
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAG
GTGTGTTATTTTGTGATCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA
GGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCATGGCTTTTTCACACAGTTA
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTAGGAGCAGTATTGAGTGGCTGTACACTTTTGGGCAACTA
AAAAGGCTTCAAACGTTTTTGTGATGATTTCTTTTTCAGGAAACATTGTGCTCTAACAGTATGACTATTCTTTCCCC
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTCTCATTTTGAATAGAGTTT
GTGTGTAATTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTGATGTTTGT
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT
ACCCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAACTTTTCAGTT
CAGGGCAAAATGTTTCATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA
TTATGTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTGTGACTTGACAAGGCAAAACATGACAGTGGAT
TCTCTTTACAAATGGAATAAAATCCTTATTTTGTATAAAGGACTTCCCTTTTTTGTAACTAATCCTTTTTTAT
TGGTAAAAATGTAAATTAATGTGCAACTTG

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FIGURE 2

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYFPVGP GTGFLYLVN
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF
KACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPA
SMRRAADQNGGGGRHNWGQGFRLGDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 3

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTCAAATGCACGGATT
CTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGAAGTCCTGAGCGCTCAAGTTTGTCCGT
AGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCC
CCGAGTCTTTGCTGCCGAAGCTGTGACTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGT
CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAT
TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAATACC
AGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGT
GCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTT
TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAAT
TGCAGGAGCTGTACGGGAAGTCTTTTATAGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCATAATTGG
AGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTCAAGGAAAG
AAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAAGAGTGGAAAGGCAGACTACAAGTTACTGAGCA
CCTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCT
AAACCTTCCTAGAAACCCTTCAGTAATAGATAAACAGACAAGGACTGAAGAGTCTGAACTTGAAGTCACTG
GAGAGCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGCTGACAAATT
TAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGCTTTTTCTTTCTTTTAACTAAGAATGGGGCTGTT
GTACTCTCACTTTACTTATCCTTAAATTTAAATACATACTTATGTTTGTATTAACTATCAATATATGCATACAT
GGATATATCCACCCACCTAGATTTTAAGCAGTAAATAAACATTTGCAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFQKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDAVQSAHRAATRGFIRYGWRGWRTAVFVTIFN
TVNTSLNVYRNKDALSHEFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRQLQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
```

Important Features:**Signal Peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 5

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC
GTGGGCGTTTGAGGAAGCTGGGATACAGCATTAAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC
TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCTG
CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA
ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTTCCTTCATGATAAATGCTGTATCCAATGCTCAGG
TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT
TGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC
CGGGACTAGCTGTGTTTTTCAAATGCACTTATATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAG
AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATC
TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT
TTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTATATAATACAAGACTATATG
AATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAAGTTGATCTACTCCCTGAGCCAGGGTTACATCA
TCTTGTCATTTTAGAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT
TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCATC
TACTAAAAATACAAAAATAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGG
AGAATCGCTTGAACCCGGGGGGCAGAGTTGCAGTGAGCTGAGTTTGCGCCACTGCACTCTAGCCTGGGGGAGAA
AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT
CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTTCAGCAAGTTGTAAGTTATTTTGGCCTAAAAATGAGGT
TTTTTGGTAAAGAAAAATATTTGTTCTTATGTATTGAAGAAGTGTACTTTTATATAATGATTTTTTAAATGCC
CAAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

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FIGURE 6

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWIMIDAADVYPKPEQLNHAFHTCGVFSTLAFFMINAV
SNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF
GRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 7

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTTCGCCTATACCTACTGTAGCTTCTCCACG
TATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTTCTTC
CACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAACAGTGGAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA
TGCTCCTTGTCAACAATGTATACATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTA
GTGAAGTATTCTGCCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTG
AAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT
TCCTGGAAGGAATTCTCTGATTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCTGGATAACTTGATTGTC
TTCTATGTCCTGTCTTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTT
CTATTCAAGGATAGTGCTGAAGAGGCGCTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT
GTGGCCTTGACTGCCGGGACTAAAACTTACAGCACAACTTGGCAGGACGTGGATTTTCATCAGCATGCCTTTTTTC
AGCCCTTCCAATTCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT
TTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT
ATAGTCCAGTGTTTTATTTCTCAATGGCTAATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCACT
GAAAGCATCTTCATACAGAACAGCAAACCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCTTCAG
AGGAGTAACCGTGATCAGATTAAGAACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCCCTTATTTTT
GTAAGTGCATTCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCTGGATAACATGTTCCATGTCTTGATGGCC
CAGGTTACCACTGTCTTATCACAACAGTGTCTGTCTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTG
GAAGCCCCATCAGTCTTCTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTCCGGAATACGCACCTAGG
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAGACTT
ACCAAACCCAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC
CTTATTTTTCATTTTTTCAGTGTGTTGTAATATTTATCTTTTCACTTTGATAAACAGAAATGTTTCTAAATCCTAA
TATTTCTTTGCATATATCTAGCTACTCCCTAAATGGTTCATCCAGGCTTAGAGTACCCAAAGGCTAAGAAATTC
TAAAGAACTGATACAGGAGTAACAATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT
GTGCAGATTATTTTCTTGGCCTTCAAGCTTCCAAAAAAGTTGTAATAATCATGTTAGCTATAGCTTGTATATAC
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCCCTTTTTAACA
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGTCATTTTGCAAGTAAAGAGCAACGGGACC
CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTGGGATGATGAGTCTGTGCTAA
ATATTTTGTCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTTAGAAATTCATGGGAAATTGG
ATTTTTGTAAATATCTTTTGTATGTTTAAACATTGGTTCCTAGTCACCATAGTTACCACTTGTATTTTTAAGTCA
TTTAAACAAGCCACGGTGGGGCTTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCATTACTCCTGAATTA
TTACATTTTGGAGAATAAGAGGGCATTATTTTATTAGTTACTAATTCAGCTGTGACTATTGTATATCTTTCC
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTCAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATC
CTTTCAAAGGATCACTTAGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA
AGACCAGTAATATATAAGTCACTTTACAGTGTACTTCAACCTTAAAGTGCATGGTATTTTTCATGGTATTTTG
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAATAAATTAGCAAACAAAAGTGAC
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTTAACTGGCAGGCCGTGATGTTTACAGACTAC
CATACTGTAAATATGAGCTTTATGGTGTCTTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTC
ATGCAGATGAATATAAGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATGACTGGCAAGAAAT
TGGTGGAAATTTGTAATTAATAATTTAAACCT

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FIGURE 8

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSSELVKLVFCVLVSFCVIK
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPMAMAVIFS NFSIITTALLFRIVLKRRLNWIQ
WASLLTFLSLIVALTAGTKTLQHNLAGRGFHHD AFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFS
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY
GHSAFSVALIFVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVVDFRPSLEFFLEAPSVLLSIFIYNA
SKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,
328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG
AAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTTGGTGGTTTCAGCAAGGCCTCAGTTTC
CTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT
ATAGACCCCGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA
AATATTGCGGCAGTTTTATGCATTGCTACCATTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG
AACGTTATCATCAAATTAAACAAGGCTGGCCTTGTAAGTTGGAATACTGAGTTGTTTAGGACTTTCTATTGTGGCA
AACTTCCAGAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
ATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTT
GGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA
GCAGAAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTTCGTGATTTTCAGAAAATTTCTTTA
CGGGTGAAGCCAATTTACATGGATTAACCCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG
CTACTTTCCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAGG
TTCACAGAAGTTGCTTATTCTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCT
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAGACTATG

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FIGURE 10

MWWFQQGLSFLPSALVIWTSAAFIFSYYTAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATYVRY
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLSRDI

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FIGURE 11

CCCACGCGTCCGCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGCGGAG
CCGACATGCGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCACCTTCGCCCTTGTAAGTGTGCGACGC
GACTGCCCCCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGG
CAGAGCTGCGGGAGCTCTCTGAGGTCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCT
GCGGCGCCTACCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCTTGT
TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA
GTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA
ACAGAAACAGCTTGTTTTTTTTCTTATTGTTTTTGAGACTTTTCCCATGACACCAAAGTGGTTCCTGAACCTCT
CGGCCCCAATTCTGAACATTCCCATCGTGCAGTCTTCTTCTCAGTCTTATCGGTTTGATCCCATATAATTTCA
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCCTGGGACACTGTCTTTA
AGCTGTTGGCCATTGCCATGGTGGCATTAAATTCCTGGAACCCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATGATCTGGATTTTCTGTTTGCCACATCC
CTGGACTCAGTTGCTTATTTGTGAATGGATGTGGTCTCTAAAGCCCCTCATTGTTTTGATTGCCTTCTATAG
GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTACAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC
AGGTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGTGGCCGGGCG
CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTACAAAGTCAGGAGTTCAGAGCC
AGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT
AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT
CACACCACTGCACTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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FIGURE 12

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYRKEHQAYVFLFLFCG
AYLYKQGFaipgssflnvlagalfgpwlglllccvltsvgatccyllssifgkqlvvsyfppdkvallqrkveenr
NSLFFFLFLRLFPMTpnwflnlsapilnippiqfffsvliglipyNFICVQTGSILSTLTSLDALFSWDTVFKL
LAIAMVALIPGTlikfsqkhlqlnetstanhihsrkdT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

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FIGURE 13

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG
GGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA
TGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCA
TGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT
CTTGACCATGTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA
AAATGAACCTGTGTGTAATTCTGTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCA
ATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA
AACTAGGAGATCCCTTTCCATTCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTG
GTGTGATTGGAGTGACTCTCATGGCTCTTCTTCTGGATTTGGTGTCTCAACTGCCCATACACTTACATGTCTT
ACTTCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG
GTTTCTGGGGAATGATAAAAAGTGTTACCCTTCAGCATCAGGAAGTGAAAATCTTACTCTTATTCAACAGGAAG
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAG
AATACTCCAAAACCTTCAAGGGGAAATATTTTAAATTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAA
TTTTCATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCATTGAGATCA
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATTTCTTTCATTCTTGTGGAATAA
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCT
CCAATGTCATTGTCTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGA
GTATGCCCTTGAATAACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGT
TTGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCAGAGA
AGCAAAATGGCACCTTGAACCTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAAATTTAGATATAAGAGG
GGGAAAAATGGAACCGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGC
ATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAA
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAAAG
GTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTA
AGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATTAAATCAGAGACTGTAACAAAAA
AAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTTGTTTTATTG
CAGCTTATAATG

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FIGURE 14

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVLNSSSRYPFW
KMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDPPILSPKHGILSIEQLISRV
GVIGVTLMAILSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS
GFWGMKSVTTSASGSENLTLLIQQEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWK
IFMATINIVFDRVGKTDVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS
SNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSAISSILFLYLAHKQAPE
KQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 15

GACGGAAGAACACGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGAACATCGCGGCC
CAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTGCTGCCGCCGCCGCCGTGCCCTGCC
CACAGCGCCACGCGCTTCGACCCCACTGGGAGTCCCTGGACGCCGCCAGCTGCCCGCGTGGTTTGACCAGGCC
AAGTTCCGCATCTTACCACTGGGAGTGTTTCCGTGCCAGACTTCGGTAGCGAGTGGTTCTGTGGTATTGG
CAAAAGGAAAAGATACCGAAGTATGTGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGATTTT
GGACCACTATTTACAGCAAAATTTTTTAAATGCCAACCAGTGGGCAGATATTTTTTAGGCCCTCTGGTGCCAAATAC
ATTGCTTAACCTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGTGAGAATATTCGTGGAACCTGGAATGCCATA
GATGAGGGGGCCCAAGAGGGACATTGTCAAGGAACTTGAGGTAGCCATTAGGAACAGAACTGACCTCGCTTTTGG
CTGTACTATTCCCTTTTTGAATGGTTTTCATCCGCTCTTCCCTTGAGGATGAATCCAGTTCACTTCCATAAGCGGCAA
TTTCCAGTTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCTGAGTTCTGTGTCCGAT
GGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTTATATAATGAAAGCCAGTT
CGGGGCACAGTAGTACCAATGATCGTTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCGAT
GATCGTTATAACCCAGGACACTTTTTGCCACATAAATGGGAAAACCTGCATGACAATAGACAACCTGTCTGGGGC
TATAGTAGGGAAGCTGGAACTCTGTACTACTTTACAATGAGAATTTGGTGAAGCAACTGTAGAGACAGTTTCA
TGTGGAGGAAATCTTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGAGGAGCGACTG
AGGCAAGTGGGGTCTCGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTATACCTGGCGATCCCAGAATGAC
ACTGTCACCCCGAGTGTGTGGTACACATCAACAGCCTAAAGAAAAATAGTCTATGCCATTTTTCTTAAATGGCCC
ACATCAGGACAGTGTTCCTTGGCCATCCCAAGCTATTCTGGGGCAACAGAGTGAACACTCTGGGCCATGGA
CAGCCACTTAACTGGATTCTTTTGGAGCAAAATGGCATTATGGTGAAGACTGCCACAGCTAACCTATCATCAGAT
CCGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT
ATGTCATAAGGCTAGGAACATCAGGTGCTATAATTGTAGCAGCATGGAGAAAGCAATGTAACTGGATAAGAAAA
TTATTTGGCAGTTGACCCCTTTCCCTTTTTCCCACATAAATTTTTCTTAAATACCCATGTAAACCTTTTAACTCT
CCAGTGCACTTTGCCATTAAAGTCTCTTCACTTGATTGTTTCCATGTGTACTCAGAGGTGAGAATTTTTTCA
CATTATAGTAGCAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATGAT
TATATAGTTATGATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTTGTCCAA
CATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCTTACTACACAGCTAATGTGTATGGTATAGACTGTTG
CTCCTAGGCTACAGACATACAGCACTTTACTGAATACGTGAGGCAATAGTAACAGTGGTATTTGTATATCGAA
ACATATGGAACATAGAGAAGGTACAGTAAAAATACGTGAAAATAAATGGTGACCTGTATAGGCGACTTACCAC
GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCCTAGGACATTATTGAA
CACTGCCAGAGCTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTTCTCAATT
ATAAATTAACATAAGTGTACTGTAACTTTTACAAACGTTTTTAATTTTTTAAACCTTTTTGGCTCTTTTGTAAATAAC
ACTTAGCTTAAACATAAACTCATTGTGCAAAATGTAA

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FIGURE 16

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHGVSFVPSFGSEWFW
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW
NAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLEFWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVL
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKL
SWGYYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS
QNDTVPD VWYTSKPKEKLVYAI FLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISLEQNGIMVELPQLTI
HQMPCKWGWALALTNVI

Signal sequence:
amino acids 1-28

N-glycosylation site.
amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.
amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.
amino acids 361-369, 389-397

N-myristoylation site.
amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.
amino acids 410-432

Alpha-L-fucosidase putative active site.
amino acids 283-295

FIGURE 17

[illegible]

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FIGURE 18

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
VLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT
SDLFATQDPQIEKTFEVNVLAFHWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYCSSK
FAAVGFHKTLTDELAALQITGVKTTCLCPNEVNTGFIKNPSTSLGPTLEPEEVVNRLMHGILT
EQKMI FIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 19

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGAT
GCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGTAG
CGCCCGAGTGTCTGGGGGGCGCACCCGAGTCGGGGCCATGAGGCCGGAACCGCGCTACAGGCCG
TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG
ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTATAAAG
TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA
GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAAAAGTTCA
TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC
AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGACTGATGGCAGCATATCACAATTTA
GGAAGTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATGTACCATCAGC
CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA
TGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG
AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA
AAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA
TTCCCCTTCTCCTCCTCCTTGTGGTCACACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA
GAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC
AGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACAAAGCGAAGCTGACTTAG
CTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTCCGGGAGAAGCCACTCCCG
ATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC
TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCCAGACCAAATGG
GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTATTAGGACATATAAAAAA
CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA
TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA
CCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC
TTATGAGAAGGTACCTTGCCCGAGTCTGGCACATAGTAGAGTCTCAATAAATGTCACTTGGTT
GGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC
TTGGAAAACCACTCTGTTTTCTTGCTCTATACAGCAGCACATATTATCATACAGACAGAAA
ATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAGGTTGGCCTGTGCATCGGCAATTCTC
ATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAAAA

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FIGURE 20

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRLN
FEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGDWIGLRRREEKQSNSTACQDLYA
WTDGSISQFRNWWYVDEPSCGSEYCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE
KPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLVVTTV
VCWWWICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDLKNISF
RVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE
IYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 21

AGGCTCCCGCGCGCGGCTGAGTGGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCGCGACGCTGGGACTCCTGCTGCTGGTCTGCTTGGGCTTCCTGGTGCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTTACATCTGCAGTGAGATGGACCTCGGGGGCTTGGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGCTGGTGCCACTCCAGTACAAGCGTGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAATGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGTGGTTTGAATCTGCTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
TCGGGTACATTTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGTT
ACACCGTGTGAGGATCTTGGTGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTCTTGGAAATCTCTATCTGAATGATTACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTCAGAGGTTTGGCCTGGACAAATGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGG
GTAGCTTGTCCATCAGCTCCACGCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAAAGACGCTTTACCTCCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTCACTGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTACGGAAACCCCC
ACCTGGGCAGGAACCACTACATTAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCTGTCTCAGCTCAAACCCCTAAGCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTTGTTGATGATGGCTTTCTACAGCCCTGCTCTTGTGCGGAGGCTGTGCGGCTGTCTTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGACGTCACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTGTGCTTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCAACAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCACAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCCCGAACAGCAGGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACA

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FIGURE 22

MTTWSLRRRPPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI
FGGSIHYFRVPREYWRDRLLKMKACGLNTLTYYVPWNLHEPERGKFDFSGNLDLEAFVLMMAE
IGLWVILRPGPYICSEMDLGGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQYKR
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKDGLSKGIVQGVLATINLQ
STHELQLLTFFLNFVQGTQPKMVMEYWTGWFD SWGGPHNILDSSSEVLKTVSAIVDAGSSINLY
MFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSISGIPLPPPD
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYETSITSSG
ILSGHVHDRGQVFVNTVVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL
IGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSISSTPCDTFLK
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG
RNQYIK

Signal sequence:
amino acids 1-27

Casein kinase II phosphorylation site.
amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.
amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

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FIGURE 23

[illegible]

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FIGURE 24

MNSSKSSETQCTERGCFSQMFLLTVAGIPILFLSACFITRCVVTFRI FQTCDEKKFQLPENF
TELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQEF
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLED CATMRDSSNPR
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:
amino acids 1-42

N-glycosylation site.
amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.
amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.
amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 27-38

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FIGURE 25

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC
TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG
AGCAAAGCCGGGCTCGGCGGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA
CACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCC**ATG**GCTCCCAAGA
AGCTGTCTGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG
ACACTCGGTCTGTTCTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCCCGTTCC
GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCGGACCGGCTTT
TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTACCACGAGC
CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGAATGAGGCAG
CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG
GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT
TCCTTGCCGCGAGTGGACTCCTGGTTCAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC
ACAATGGGGGCAACATCATTAGCATTCAAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG
ACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGGAGAAAAGATCTTG
TCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG
TAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTTCGGAAGTATGAACCCC
ATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT
CCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG
TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG
GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC
CCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGTTCAGGAAGTTCCTTTGGGAC
CTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTGACTCTGCACCTGGTTGGGCATT
TACTGGCTTTCTAGACTTGCTTTGCCCCCGTGGGCCCATTCAATCAATCTTGCCAATGACCT
TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATAACATTT
TTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG
ATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAGAGACAACTATTTTGGACGGGGAAAC
TGGGGTCCAAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA
GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTGGGGCAACAATCCTTACCCAGTGGATGA
TGTTCCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCCTCCAGTTGCCAAAATGGC
CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG
TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA
ACTTGGGCGGTACTGGACAAAGCAGGGGCCACAACAGACCCTCTACGTGCCAAGATTCTCGC
TGTTTCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAAGTAGAAGATGTACCTCTCCAGC
CCCAAGTCCAATTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA
TCAATTCCTTTTCTAGCTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCAC**TGAA**
AGGTAGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTG
GATTACCTGAGGTGAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA
AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTG
AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGAGGTTGTACCACTG
CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAAAAA

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FIGURE 26

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVLW
ADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA
EWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS
YRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIFTLLR
KYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNFGYWNG
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMLGPVTLH
LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPNNGVHDRA
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKPPILGQTIL
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYLPGWTKGQVW
INGFNLGRYWTQGPQQTLVVPREFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL
HRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648**Tyrosine kinase phosphorylation site.**

amino acids 191-198

N-myristoylation site.amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 27

[illegible]

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FIGURE 28

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGHGKDLLNGVKLVVETPEETLFTYQG
ASVILPCRYRYEPALVSPRRVRVKKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQDKE
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA
EQAAVVASFQELFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRL
HRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW
LADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.amino acids 36-42, 184-190, 208-214, 237-243, 297-303,
307-313

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FIGURE 29

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAAGTCCCCTGGCAGTCTGGTGCTGTTG
CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCCGCGTCATCACGGACGAGAAC
TGGAGAGAAGTCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT
CAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT
ACTATTTATCATTTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC
TTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATGGTTTGGT
CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG
TGCCATAACTACTTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT
TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT
TGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAATTATTATCAGAA
TCTGCACAACCTTTGAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA
GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGCCATAAGACAACGC
TCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA
TGATTTTGATAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTGAAGTGTGACTTTTTT
GAATATTGCAGGGTTCAGTCTAGATTGTCAATTAATTGAAGAGTCTACATTCAGAACATAAAA
GCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA
ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAATAATAACCTATTTT
AAGTCTGAGTTTGAATTTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT
ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTGTTTCACTGTGTGAAAAAAG
AAGATATTTCCCATAAATGGGAAGTTTGGCCATTGTCTCAAGAAATGTGTATTTTCAGTGACAA
TTTCGTGGTCTTTTTAGAGGTATATTCCAAAATTTCTTGTATTTTTAGGTTATGCAACTAAT
AAAACTACCTTACATTAATTAATTACAGTTTCTACACATGGTAATACAGGATATGCTACTG
ATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
ATTTTTCTTACTTACTATGGGTACATTTTTTATTTTTCAAATGGATGATAATTTCTTGGA
ACATTTTTTATGTTTTAGTAAACAGTATTTTTTGTGGTTTCAAAGTGAAGTTTACTGAGAGA
TCCATCAAATGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTTCAGATTTTACATC
ATTCTTGCTGAACCTCAACTGAAATTGTTTTTTTTTCTTTTGGATGTGAAGGTGAACATT
CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTGAAAATTCAAAGAAGCTT
AATATAAAAGTTTGCATTCTACTCAGGAAAAAGCATCTTCTGTATATGTCTTAAATGTATTT
TTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGATGTTTTAAA
TAATAACATTTTTATATTTTTTAAAAGACAACTTCATATTATCCTGTGTTCTTCTGACTG
GTAATATTGTGTGGGATTTTACAGGTAAGAGTCAGTAGGATGGAACATTTTAGTGTATTTTA
CTCCTTAAAGAGCTAGAATACATAGTTTTTACCTTAAAGAAGGGGAAATCATAAATACAA
TGAATCAACTGACCATTACGTAGTAGACAATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGT
TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCC
TTTAGAATTTAAATATTGTACCATTAAAGAGTTTGGATGTGTAAGTGTGATGCCTTAGAAA
AATATCCTAAGCACAAAATAAACCTTTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAA
AAA

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FIGURE 30

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLQ
PEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINF
ISDKEWKSIIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSEEEAE
SKEGTNKDFPQNAIRQPSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

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FIGURE 31

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTCCGGTGCCGCGACTTTCACGATGGC
TCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAAAC
TGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT
GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT
TCTTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTCCCTGATGA
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG
ATGAGGAAGTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTA
ATGACTGCCAATCATTTGCCCCATCTATGCTGACCTCTCCCTTAAATACAAGTGTACAGGGC
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA
TCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA
AGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCCCTCTCCTGTCAATTCCAGGCTCTTTCCAT
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGG
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC
CTGCCATGCTGTGGCCAAGTGTTCAGTGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA
AATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATCAGCTATTGAGACATCTCCA
TGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTT
AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCCAAG
GACTCTTGCTTCCCTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAGTATAAGCCTAA
CTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTATCATTGAAGACAATATT
GAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT
GTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCACCTAACCCCTCTGACATACTCCCCACAC
CCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATTTCCTTTTG

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FIGURE 32

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFDW
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNCTGL
NFGKVDVGRYTDVSTRYKVSTSPSTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENV
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

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FIGURE 33

CGGACGCGTG GGGGTG CCGGAC ATGGCGAGTG TAGTGCTGCCGAGCGGATCCCAGTGTGCGGCG
GCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAG
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGAGCTACTGAATCCC
AACAGGCAGACCATTATTTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGTTGCTG
AATTTTTCTAGCAGTGAAC TCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA
TACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGTCCTGGTC
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCTGCG
GTCCTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT
CAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGAGTTAACATGTGAA
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACTGGGTGAGAGTCGATGATGAAATGCCTCAA
CACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACA
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC
GATCCCCCACAAC TATCCCTCCTCCCAACAACCACCACCACCACCACCACCACCACCACC
ACCATCCTTACCATCATCACAGATTCCTGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAAC TCCGAAGAA
AAGAAAGAGTACTTCATC TAGATCAGCCTTTTTGTTTCAATGAGGTGTCCAAC TGGCCCTATT
TAGATGATAAAGAGACAGTGATATTGG

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FIGURE 34

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIP TGDGQNLFTKDVTVIEGEVATISCQ
VNKSDDSVIQLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSE
VEEWSDMYTVTSQMLKVKHEDDGVFVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ
GLTREGDALELTCEAIGKPQPVMTWVRVDDEMPQHAVLSGPNLFINNLNKT DNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHA VIGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

N-myristoylation sites.amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

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FIGURE 35

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCTCAGGAGGAGACAGCCTCCCGGCCCGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCCGTGAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCGGGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCCGCTCATGATGGCCCGGCCAAAAGGGCATTCTTACCTGACCCCTTTTCTCATCTCTGGGGACATGTACAC
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTTACAGTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCCTCGTA
TCAAGAATTTCCAGATAAACAACCAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC
GGGCCTCCCATTCGAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAGAAACTCCTGGAACTG
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTCTGGGACTGACTGGATTTTCTACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTGTGTGGCCCTTGGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCCACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCCACAGAACACCTGAACCTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGCGAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTGTGTT
TAATTAGGGCTATGAGAGATTTCAAGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCTTGGACCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCTAC
TGGTCTCATTTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCAGTGTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTCTTTTGACTCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCAATTTCTTTTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAGCCT
CGGCTGAGTGAGGGAAAGCCAGCACTGCTGCCCTCTCGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT
CACCTTGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTCTATTTGAAGCGATTAACTGTGTCTAATGCA

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FIGURE 36

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGFYLTFLILGTCTLFFAFECRYLAVQ
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCWPVGNVCVGKRNRYFYLFIL
SLSLTTIYVFAFNIVYVALKSLKIGFLETLPKTPGTVLEVLCFFTLWSVVGLTGFHTFLVAL
NQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

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FIGURE 37

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCCGCTCACTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGCGAGCCCCGCCGCGCCAGGCGCCGGTGCGCAGCTGC
TGCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCG
CCCGCCCTTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGCAGCACCCGGCCCCCGCCGGCGAGCCTGGCTACAGCTGCACCTGCCCGCCGGGATCTCCGGCG
CCAATGCCAGCTTGTTCAGATCCTTGTGCCAGCAACCCCTTGTCAACATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTGCAATGAAGGTATGAAGTCCCAACTGTGAACAGGCACTTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCCCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCCGCAAGATGCCACTGCCTCACTGATTTTGC
TCTGGAAGGTCACGGCCACAGGATCCAACAGTGCTCCCTCATAGATGGACGAAGTGTACCCCTTCAAGCTT
CAGGGGGACTGGTCTCCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTCTGGTGGTGAAGGTGAGCACCTGTGTGCCGGGGGAGAGTCAG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACGCCAGCT
GTATTGATGCAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCAGCTGCCGCAGCGTGGGCACCACT
ACAACTGCCTCTGTGATCCAGTTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGCTGGCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTGAGTGTCTGAACGGAGCCACCTGTGACAGCGACGGCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTCAGGTGAAGAGTGCAGACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCCTGGACAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCACATGCCACGGCACTCCC
TCTACATCATCATTTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGCAGCATCGACAGCG
AGTTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGTTTGGAAAGAAATCCCGGCCCTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCTCTGATGACAAACCTTGGTCACACTGATTAATAACTAAAGATTTGTAAT
CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAATAAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAAATATTTTAAAAACAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGTGAGTGGCGGCTTCTGAGTAGAGTTAGGAAAACAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTGTTTTGTGGAAA
AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAAGTAAC
TTATTTCTGCAGTGTGTTGTTGAACCTTTGTGGAAACATTCTTTGAGTTTGTGTTTTGTGATTTTCGTAACAGTCG
TCGAACTAGGCCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTTCTGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGATTGATTGATATGTGCTTCTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

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FIGURE 38

><subunit 1 of 1, 737 aa, 1 stop
 ><MW: 78475, pI: 5.09, NX(S/T): 11
 MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP
 EPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICNEG
 YEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKVVEM
 KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQQCSL
 IDGRSVTPLQASGGLVLLLEEMLALGNHNFIFGVNDSVTKSIVALRLTLVVKVSTCVPGESHAN
 DLECSGKGKCTTKPSEATFSCCEEQYVGTFC EEYDACQRKPCQNNASCIDANEKQDGSNFTC
 VCLPGYTGELCQSKIDYCI LDPCRNGATCISLSGFTCQCPEGYFGSACEEKVDPCASSPCQN
 NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGT SYKCLCDPGYHGLYCEE
 EYNECLSA PCLNAATCRDLVNGYECVCLA EYKGT HCELYKDP CANV SCLNGATCDSDGLNGTC
 ICAPGFTGEECDIDINECD SNPCHHGSGCLDQPNGYNCHCPHGWVGANCEIHLQWKSGHMAES
 LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA
 IASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568**Glycosaminoglycan attachment site.**

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571**Amidation site.**

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

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FIGURE 39

GAGCGCCGCGCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCCGGCCCCCCCCACCCACGTCGT
CGTTGCTGCCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCTCC
GCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTTGCGGGGGCT
TCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTGCTGC
TAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGTTCGGCC
TGGTCATTGCAGTGGGCATCTTCTTGTTCCCTGATTGCTTTAGTGGGTCTGATTGGAGCTGTAA
AACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATTGTTTCAGT
TTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCTGGAGGTTG
GTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCTGTGGGTTCC
GAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCACTCGTGCTCGC
CATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGGTGGCATTGGCC
TGTTCTTTCAGTTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACAGGAACCAGAAAG
ACCCCCGCGCGAATCCTAGTGCATTCTTTTGAATGAGAAAACAAGGAAGATTTCTTTTCGTATT
ATGATCTTGTTCACTTTCTGTAATTTTTCTGTTAAGCTCCATTTGCCAGTTTAAGGAAGGAAAC
ACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTACTCTATGTTTCTCTACA
TGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTTGGTCTCTGAAGCTCGGTGGCAC
CTGGAATTTACTGTATTCACTGTGCGGGCACTGTCCACTGTGGCCTTTCTTAGCATTTTTACCT
GCAGAAAAACTTTGTATGGTACCCTGTGTTGGTTATATGGTGAATCTGAACGTACATCTCAC
TGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTACTGGAAAAAGAGTGGAAATT
TATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAATCCAAATTTCCCAATTTTTTT
TGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTATAAAAATGATAATTTACTTGT
AGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTATGTCTTAGGAAATTGTGGTTTTAA
TTTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTTTCATGAAATGTTCTAATGTATAAT
AACATTGACTTTACGCTCCATCAGAATGGAACGAGTTTTGAGTAATCAGGAAGTATATCTAT
ATGATCTTGATATTGTTTTTATAAATTTGAAGTCTAAAAGACTGCATTTTTTAAACAAGTTAG
TATTAATGCGTTGGCCACGTAGCAAAAAGATATTTGATTATCTTAAAAATTGTTAAATACCG
TTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTTGTCAAACCTAAGCATATTTGAATATGA
TCTCCCATAAATTTGAAATTGAAATCGTATTGTGTGGCTCTGTATATTCTGTTAAAAAATTTAA
GGACAGAAACCTTTCTTTGTGTATGCATGTTTGAATTTAAAGAAAGTAATGGAAG

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FIGURE 40

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALVG
LIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQRNL
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVGGIGLFFSFTEILGVWLTyr
YRNQKDPRANPSAFL
```

Signal Peptide:
amino acids 1-34

Transmembrane domains:
amino acids 47-63, 72-95 and 162-182

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FIGURE 41

CAGTCACCA**ATGA**AGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC
TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTGTAGACGCTGCAGTGTGAGGGACCTGTCT
GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC
AGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCTATGACTGGCTGATCC
TCCAAGGTCCAGCCAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCTGGC
AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC
CTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG
GCATCTTCCAGAGCCCTGGTCCCTGGGATCCCAGAAACAGCATCTGTGTGGCTATCACAGTCC
AAGAAGTGTTCAGAGCCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAGCAGGAAGCC
CCATGACCCTGAGTTGTTCAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGCCTCCTCTTCT
CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATCCAGATCCCCA
CAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT
GGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCA
CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGAGGAGGCCCCCTGGGC
CTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC
CAGATCCTCATCTGTATCACAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC
TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA
AGGCTACTGCTGA**ATGA**AGTAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATC
TGATTCTTTATTTTCTCTTCTCCTGTCTGCACATATGCATAAGTACTTTTACAAGTTGTCCAG
TGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG
TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCAGGAATTT
CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC
AGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT
TGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA
GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCACAAACGAAAAATAA
TCTGGCCCAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCCCTAGGTGT
TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTTCAGCTAT
TCTTACTGACATAACAGTCTTTAGCTGGTGCTATGGTCTGTCTTTAGTTCTAGTTTGTATCC
CCTCAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTT
GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAA
GGCCCCAGAGAGCTAACTCACCTTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG
AGAACCACAAAAACAGCTGTCGCCAAACACCGACTCTGTCGTTGCCTTGATCTTGAAGTCCAG
CCTCCAGAACTATGAGAAATAAAATCTGGTTGTTGTAGCCTAA

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FIGURE 42

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359.aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

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FIGURE 43

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCAACAAACGGGACCCTTC
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGGAA
GGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAACTCTGGGTGTCTGCATT
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCCTCACCTCTATTGGGCA
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT
GGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAA
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCCTGTGAATGCCTACAACTGGTGAAGCG
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTCAGGACTCAGCTGCAGTTTTAT
CGCCAACCTCTCTGTGCAGCGGCAGTTCTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACT
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC
CTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT
CCAGTTGGGTGATCTGCACCGTGGCCTGGAGCTACCCGCCGCTGCTCTCCCTTGACCCAAG
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCATCTATGAGAGGCCTGT
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGGAGGGTGTCAAACCTGAC
ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACTATGGCAACAGGGCCCCACAGCTGCT
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAACTTGCACGAGCCAC
CGTTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTACCGGGTTTCCAAAAGCTCCTG
GCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAAACAGAGGGGAATAGGTT
AGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA
CTGACATCCTTTTCTGTCTTCCCCTTCCCTGGTCTTCAGCCCATGTCAACGTGACAGACACC
TTTGTATGTTCCCTTTGTATGTTCCCTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGA
GCAGAGGGAGACCATAGGGCGACTCCTGTGTGACTGAAGTCCAGCCCTTCCATTTCAGCC
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC
CTAGCAAGGTGCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC
TGATACCTTGTTTACATGTTTGTGTTTTATGGCATTTCTATCTATTGTGGCTTTACCAAAAAAT
AAAATGTCCCTACCAGAAAAA

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FIGURE 44

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD
EDEIGAALKMRLQDTYRLDPGTISRGEIPGTTYQAMLSVDDCFGMGRSAYNEGYYHTVLWM
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLRYFEQ
LLEEREKTLTNQTEAELATPEGIYERPVLDYLPEDVYESLCRGEVGLTPRRQKRLFCRYHH
GNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEIEIERIKEIAKPKLARATVRDPKTGVLTVAS
YRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSRRPFDG
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYRTRHAACP
LVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

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FIGURE 45

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG
CGGCGGGCGCGGGTGCAGGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCCAGCC
TGTCTGTGTCGTCGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTCACACCGATCCTGGGC
TTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGGG
TCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA
GGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATCTCCCTCTCTCCAGGTGTGA
GCAGCCTATCAGTCACCAATGTCGCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTCTGC
TGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATGTTTTACCA
GAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGGCTGCCCTCTTGAGG
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT
TCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAAGATTGTA
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTAAATATTGGGCAGCGCCGATTTAATTTAC
AGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG
GCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAAAACTTTACATCAGCCA
AAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTAATTCCAATACAGGAAAAG
CCTTGAAGCATACTGCTCAGAAATTCCTTACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAACTGG
GGATGGTTTCAAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGGAATAATGGCTTCTTCTCTT
ACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA
CTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG
ATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG
CCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC
AGCGCACGGAGTTCAGTTTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTATCAGAA
ACATCCGCTATATGAGTGGTGGAACAGCTACTGGTGATGCCATTTCTTCACTGTTAGAAATG
TGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGT
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC
ACGCTTTCTTACAAAGAGAGTTCACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA
TTTGTAGAGATTTCTTAGAATCCCAGCAATAATGGTAACATTTTGACAACTGAAAGAAAAAGT
ACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT
CAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG
CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT
GGCTCTTAGAAACTCAGGAAAGAGGAGATAATGTGGATTAAAACCTTAAGAGTTCTAACCATG
CCTACTAAATGTACAGATATGCAAATTCATAGCTCAATAAAAGAATCTGATACTTAGACCAA
AAAAA

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FIGURE 46

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEF SVYG
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTKG
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRFRNLQKNFVG
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLF AIKEVGFRGGNSNTGKALKHTA
QKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV
TFVDKAVCRNNGFFSYHMPNWF GTTKYVKPLVQKLC THEQMMCSKTCYNSVNIAFLIDGSSSV
GDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRT EFSFTDYSTKENVLAVIRNIRYMS
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITIFSVGVAWA
PLDDLKDMASKPKESHAF FTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532**N-myristoylation site.**amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449**Amidation site.**

amino acids 145-149

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FIGURE 47

CCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCC**ATG**GGGGCCTGCCTGGGAG
CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT
GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAGTTCTTCCTCTTCCTGG
GGGTGCTGGTGTCATCATATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT
GGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC
TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGGCCTTCTTCTTCTTCTTTT
TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT
TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACATCCCTGACG
GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCATCCTCATCC
AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG
AGTGCGATTCCCGTGCTGCTGACGAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT
CGATCGCGGCGGTGGCGCTGATGTTTCTGTACTACACTGAGCCCAGCGGCTGCCACGAGGGCA
AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCATCGCTGCTGTCTGCCCCA
AGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATCACCTCTACACCA
TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA
CCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATG
CCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTTCATCAGTCTGCGCTCCT
CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA
CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG
GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCTGGCCTCACTGCACGTCTATGA
TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG
TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC
CACTCCTCCTGCGCAACCGCGACTTCAGCT**GAG**GGCAGCCTCACAGCCTGCCATCTGGTGCCTC
CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC
AGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTGCCCCTGAGCCGGGCCTTCTAGTCGT
AGTGCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC
ACGGTGGAGCTGCCTCTTCCTTCCCCTCCTCCCTGTTGCCCATCTCAGCATCTCGGATGAAA
GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACC
ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTACGTCCCCCAGGGGACCCTGCC
CCCTTCCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAACAAGCCAGTGCG
TGTAATAAAAAA

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FIGURE 48

MGACLGACSLSCASCCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVES
QLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFILIQLVLLIDFAHSWNQR
WLGKAEEDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVS
IAAVLPKVQDAQPNISGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA
FDNEQDGVTSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLY
LWTLVAPLLLNRNDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

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FIGURE 49

GCCGCGCGCTCTCTCCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGCGT
GGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGGATTCCAGGGCTCCTCTTCCTTCTCTT
CTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCCACTTGGCC
TGCATACCGCCTCCCTGTCGTCTTGCCCCAGTCTACCCTCAATTTAGCCAAGCCAGACTTTTG
AGCCGAAGCCAAATTAGAAGTATCTTCTTCATGTGGACCCAGTGTCTATAAGGGAAGTCCACT
GCCCCTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGGCAGCCG
CACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAACACCGAGA
CTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGCAGGTTTAC
CATTTTTGGGAAGGACTTCCTGCTCAACTACCCTTTCTCAACATCAGTGAAGTTATCCACGGG
CTGCACCGGCACCCTGGTGGCAGAGAAGCATGTCCTCACAGCTGCCCACTGCATACACGATGG
AAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCCAAGTTTAAAGA
TGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCAGCAGATGAAATTTTCACTGGAT
CCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCAATGACATCGGCAT
GGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAATTTATGAAGATTGG
GGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTCTGGTTATGACAATGA
CCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGACCTATGACTTGCTCTA
CCAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGGTCTATGTGAGGATGTGGAAGAG
ACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGGGCACCAAGTGGGTGGACAT
GAATGGTTCGCCACAGGATTTCAACGTGGCTGTGAGAATCACTCCTCTCAAATATGCCCAGAT
TTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGGTGACACAGTGTTCCTCCTG
GCAGCAATTAAGGGTCTTCATGTTCTTATTATTAGGAGAGGCCAAATTGTTTTTTGTCTATTGGC
GTGCACACGTGTGTGTGTGTGTGTGTGTGTGTAAGGTGCTTTATAACTCTTTTACCTATTTT
TTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACCTGGTTTGTGTATCATATCATATATC
ATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAAAAAAATACTGATTTGGGGCAATG
AGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTGCAAACTTTGATTTTTTATTTTATCTG
AACTTGTTTTCAAAGATTTATATTAATATTTGGCATAACAAGAGATATGAAAAAAAAAAAAAAAAA

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FIGURE 50

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS
SCGPQCHKGTPLPITYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRR
KRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQK
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKNANDIGMDYDYALLEL
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDILLYQQCDAQPGA
SGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYL
DCREG

Signal sequence:
amino acids 1-19

N-glycosylation site.
amino acids 93-97, 207-211

Glycosaminoglycan attachment site.
amino acids 109-113, 316-320

Casein kinase II phosphorylation site.
amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.
amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.
amino acids 171-177

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FIGURE 51

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGGCAG
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTCTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGGCCGCCAGTTTCAGCGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTATCTCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTGATAAAGGCTTCGATCTCATGTATATTGGAGG
CAATATCAATGTGATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCTACAAGTGCAAATGTAAAGAAGGATACCAGGCTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATGAACCTTCAGGTCCAATTCATGTACCAAAGGGAATGGTACCATTTTAAAGGGTGACACAGGAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCAGGACTGACAACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACACAGGGGTACAGACAGACCCTCAGAAACCCAGAGG
AGATGTGTTGAGTGTCTGGTACACAGTTGTAATTTGACCATGGACTTTGTGGATGGATCAGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGCGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGTACCTCTCGGCCGCTCATGCATTACAGGGGACCTGTGCCTGTCTCATTACGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAACACAGATCACCTTGCAGGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAGGAACCTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCAAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTGAGAG
ATTTTCATCGGGTGCATTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCCCTTCACCTCATCAGTATGATTGAGTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTGAACAATAGGTACAATAGAAGTCTTCTGTCTTTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAAATCATTAAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTTCAAT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCACTAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTTAATGTTTT
CTAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTTATTTGTAATAAAAAACACTGTTAGTAAT

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FIGURE 52

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR
CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS
CSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCVDVDECATGRASCPFRQCVNT
FGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT
CVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIIPPIITNRPTSKPT
TRPTPKPTPIPTPPPPPLPTLRTPLPPTTTERPTTGLTTIAPAASTPPGGITVDNRVQTD
QKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL
PLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK
SESQR

Signal sequence:
amino acids 1-17

N-glycosylation site.
amino acids 273-277

Casein kinase II phosphorylation site.
amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.
amino acids 199-206

N-myristoylation site.
amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.
amino acids 104-116, 186-198, 231-243

Cell attachment sequence.
amino acids 382-385

EGF-like domain cysteine pattern signature.
amino acids 75-87

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FIGURE 53

CGGGCCGCCCCCGGGCCCCCATTCGGGCCGGGCCTCGCTGCGGCGGGCGACTGAGCCAGGCTGGG
CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAGCC
CAGCTGTGAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCA
TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC
TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCCTGA
GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACAGCTGGT
GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC
GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCTGCGTGTGGCGGACGAGGG
CAGCTTACCTGCTTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCTGCAGGTGGC
CGTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACAC
GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG
GCAGGGTGTGCCCCTGACTGGCAACGTGACCACGTGCGCAGATGGCCAACGAGCAGGGCTTGTT
TGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGCG
CAACCCCGTGTGCTGCAGCAGGATGCGCACRGTCTGTACCATCACAGGGCAGCCTATGACATT
CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTGCACTGCTGGTGGC
CCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA
GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG
CAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGCTACCCCTCCCT
ACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC
CTGCTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTCTTATAGACACAATGAACA
GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTACAGTACATACA
TTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCA
TCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGACTGACTGACCCCTGCCTTATTTT
ACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTTCTCCAATGGCCGTGATACACTAGTGA
TCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTTTTCTTCTCAGACAGGGACAGTGCGGCC
TCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTCCCTCCTTCCCTGCCCTGCCCCAAGTGAA
GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCCTACCATGG
TGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGCTTGCCTCTGGCCAGCTCCTGGCCTCTGGT
AGAGTGAGACTTCAGACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGCCCCAGGAATGGA
AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAAGTGGGGGTATATT
TTGGGGAAAATAAATGTCTTTGTAAAAA

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FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKEDDGQEIA
```

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

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FIGURE 55

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTG
GCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG
TGTGACCACGTGCAATATACGCTGGTTCAGTTTCTGGGTGGCAAGAACTTGAACTGCATTT
CTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTA
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGATGACCTT
GAAGTTCCCGCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTCAGGAAAT
GACAGTGATGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA
ACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGGATGCTG
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCGCCACGTTTCCCGC
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT
GAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC
CTTGACAGACATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCAGGCCATGGACATCTCC
TTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAATTTGGGATGAAGGACATG
CGCGTGCAGACTTTTCAGCATTCATTTTGGGTCAAGCACAAGTTTCTGGCCAGCGACGTGGTC
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACCTCGCC
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC
TCCCAGGGGCTTTTCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTGACAAAG
AACC GGCGCTGCAAACCTGCTGCCCCCTGGTGATGGCTGCCCCCTGAGCATGGAGCATGGCACA
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAACTTTTTTGGGAGG
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTTGACCTCTCA
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC
TAGGAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAAGTGGCTTTCATTTAGATTGTA
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTATTAAATAAAATGCTTATTTTAGGAAA

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FIGURE 56

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
EHKEQFHYFILINCGANVDLLDILQPEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDLE
VPAYEDIFRDEEEDEEHSGNDSGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILFDYE
QYEHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGVLRHVSRH
NHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKRLQEF
ADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFLASDVVF
ATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCLCTNLVIS
QGPFYLCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAPLSMEHGT
TVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNF DLSVIELKAEDRSKFLDALISLLS

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FIGURE 57

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC
CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGCTGACGGCGTCGAG
CCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG
GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCT
TCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTGCTCCT
TCAAGTGGTTTTTGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA
ACAAATACAGGTGCCTTGCACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAA
GGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTAGGAGTCCCCTTCTCCAGA
CCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA
GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGCA
CGATCTCGGCTCACTGCAACCTCCGCTCCCGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG
AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTTGGGGCCAGCTGGCCTCGATGTACGTACGC
ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCG
CCGGCGCGCGCGCCCGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTC
ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCGAGAAAGTGGTGCTG
GTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGACGACAGCCACGCGCGC
GGGAATGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC
TTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA
GGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCAGAGTGGCACC
GCGTTATTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCACCTG
GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC
AAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAGTGAACCTCCAGAGAGACCCGGAA
GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGATCCAGATGACCCCTTGGTG
CTCCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC
AATTGGCTCTTGCCTTATAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG
GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT
GCCACTTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA
ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA
GAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTTGGATGAGTCTGTACCAGTCTCAA
GACCTGAGAAGCAGAGGCAATTCTAAGGTTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC
CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA
CCCCAGTTTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT
TGTGTGGGACCTGCACTGCCCTTTCCAGCCTGACATCCCATGATGCCCCTCTACTTCACTGTT
GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA
ACCTCTTTTTTTCCCTTCTTCAAATCCTCCACCCCTTCAATGTCTCCTTGTGACTCCTTCTTA
TGGGAGGTGAGCCAGACTGCCACTGCCCCCTGTCACTGCACCCAGCTTGGCATTTACCATCCA
TCCTGCTCAACCTTGTTCCTGTCTGTTCAATTTGGCCTGGAGGCCCTAGGGCAGGTTGTGACAT
GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCACCCACACTTATCTCCCCCAGGGCCAC
TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTGATTAGAAAAA

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FIGURE 58

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAFSSGF
GTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVFPFSRPPLG
ILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRGLIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTILFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACN
HNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIWSMSPVVDGVVIPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
YATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA
```

Important features:**Signal peptide:**

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

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FIGURE 59

CGGACGCGTG GGGCTGGGCGCTGCAAAGCGTGTCCCGCCGGGTCCCCGAGCGTCCCGCGCCCTC
GCCCCGCC**ATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGTCCCTGTGTGTGGGGTCGCAGG
AAGAGGCGCAGAGCTGGGGCCACTCTTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAGTCA
GACTGTTGCAGAGGCTGAAAACCAACCTTTGATGACAGAATTCTCAGTGAAGTCTACCATCA
TTTCCCGTTATGCCTTCACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGACCAGG
ACATTGAGTTCCAGATGCAGATTCCAGCTGCAGCTTTCATCACCAACTTCACTATGCTTATTG
GAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAAGAGTGGTGATAGGGTAAAAG
AGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTCAGAGCTTCTG
CAGTGATTCCCAGCAAGGACAAAGCCGCTTTTTCCTGAGTTATGAGGAGCTTCTGCAGAGGC
GCCTGGGCAAGTACGAGCACAGCATCAGCGTGCGGCCCCAGCAGCTGTCCGGGAGGCTGAGCG
TGGACGTGAATATCCTGGAGAGCGCGGGCATCGCATCCCTGGAGGTGCTGCCGCTTCACAACA
GCAGGCAGAGGGGCGAGTGGGCGCGGGGAAGATGATTCTGGGCCTCCCCATCTACTGTCATTA
ACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAACAAGCCAGGATTG
CCCAGAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAGAGAACAGAGCATTG
GGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGCTCCTAAAGACCTTCCTCCTT
TACCCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTGGGAACCAAACCTCCGGC
AGACCAAGGATGCCCTCTTACAATTCTCCATGACCTCCGACCCAGGACCGTTTCAGTATCA
TTGGATTTTCCAACCGGATCAAAGTATGGAAGGACCACTTGATATCAGTCACTCCAGACAGCA
TCAGGGATGGGAAAGTGTACATTCAACATATGTCACCCACTGGAGGCACAGACATCAACGGGG
CCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCACAGTGGCATTGGAGACCGGA
GCGTGTCCCTCATCGTCTTCTTGACGGATGGGAAGCCCACGGTCGGGGAGACGCACACCCTCA
AGATCCTCAACAACACCCGAGAGGGCCGCCGAGGCCAAGTCTGCATCTTCAACCATGGCATCG
GCAACGACGTGGACTTCAGGCTGCTGGAGAACTGTGCTGGAGAACTGTGGCCTCACACGGC
GCGTGCACGAGGAGGAGGACGCAGGCTCGCAGCTCATCGGGTTCTACGATGAAATCAGGACCC
CGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGCTCAGTGGTGCAGGCCACCAAGACCC
TGTTCCCCAACTACTTCAACGGCTCGGAGATCATCATTGCGGGGAAGCTGGTGGACAGGAAGC
TGATCACCTGCACGTGGAGGTACCGCCAGCAACAGTAAGAAATTCATCATCCTGAAGACAG
ATGTGCCTGTGCGGCCTCAGAAGGCAGGGAAAGATGTACAGGAAGCCCCAGGCCTGGAGGCG
ATGGAGAGGGGGACACCAACCACATCGAGCGTCTCTGGAGCTACCTCACCACAAAGGAGCTGC
TGAGCTCCTGGCTGCAAAGTGACGATGAACCGGAGAAGGAGCGGCTGCGGCAGCGGGCCAGG
CCCTGGCTGTGAGCTACCGCTTCTCACTCCCTTCACTCCATGAAGCTGAGGGGGCCGGTCC
CACGCATGGATGGCCTGGAGGAGGCCACGGCATGTGCGCTGCCATGGGACCCGAACCGGTGG
TGCAGAGCGTGCGAGGAGCTGGCACGCAGCCAGGACCTTTGCTCAAGAAGCCAAACTCCGTCA
AAAAAAAACAAAACAAAACAAAAAAGACATGGGAGAGATGGTGTTTTTCCTCTCCACCACC
TGGGGATACGAT**TGA**GAGATGGCCACCTGCAAGCCAGGAAGACGGCCCTCACCAGACACCATG
TCTGCTGGCACCTTGATCTTGACCTCCAGCCTCCAGAAGTGTGAGAAATAAATGTGTTTTG
TTTAAGCTAAA

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FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
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YAFTTVSCRMLNRASEDDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR
NKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQARIAQN
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMGVTKLRQTK
DALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKILNNTREAARGQVCIFTIGIGND
VDFRLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP
NYFNGSEIIIIAGKLVDKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVTSRPPGGDGE
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM
DGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGRDGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

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FIGURE 61

CAGGAACCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC
ACGAAGGGACGATACCAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC
TGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAAGAGACAGTTTTTTTTTGGAAAGCTAAGTC
TTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAATTGAGT
AAAGTACGCTCCGGTCACCATGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG
CTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC
CTCCGGCCGCCCCACGCCCTGCCGTGAGATCAGACCCTACATTAATATCACCATCCTGAAGGG
TGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGGTCCCCAAGG
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGCGGCAGGACTT
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGACATGGCGACCGG
CCAGTTTGCTGCTCCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTA
CAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATCCTGTACGCGCAGCC
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTAGCCCTACGGGACCGCGT
CTGGGTGCGGCTCTTCAAGCGCCAGCGCAGAACGCCATCTACAGCAACGACTTCGACCCCTA
CATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCCCTCC
CGGCTGGAGAGCTCAGGTGCTGGTCCCCTGCCCTGCAGGGCTCAGTTTGCAGTCTGTGAAGC
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATCTTGGGGAGACCCTGCTTCTATCTTGGCT
GCCATCATCCCTCCCAGCCTATTTCTGCTCCTCTCTCTCTCTTGGACCTATTTTAAAGAGCT
TGCTAACCTAAATATTCTAGAACTTTCCCAGCCTCGTAGCCCAGCACTTCTCAAACCTTGGAAA
TGCATGCGAATCACCCGGGGTTCGTGTAAATGCAGATTCTGACTCAGCAGGTCTGAGTGGGT
CCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTGATGGGGTCACTCTATGAACCACA
CTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC
TCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC
CAGGCTAGAGTGCAGTGGTGAATCTCAGTTCAGTCAACCTCTGCCTCCCGGGTTCAAGCGA
TTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATGCCTGGCTAAT
TTTTGTATTTTAGTAGAGATGGGGTTTACCATATTGGCCAGGCTGGTCTTGAACCTCTGAC
TTCAGGTGACCCACCCGCTCGGCCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
CTGGCCAATTCCAACATTCTTAAATTCTCTCATCCCTCCAGGGCTCCCCGTGCTATGTTCTCT
TTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCACTGCAGCCACCGTTTCAATTTATTCA
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAAGACACA
GGCCCTGCCCTGCCCTCAGTGACTGGCCAGTCCAGCCAGGCGGGGAGAGATGTGTACATAG
GTTTTAAAGCAGACCCAGAGCTCATGGGGCCTGTGTTCTGGGTGTTTCAAGGTGCTGCTGGTCC
TCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTC
CTTCCCGTTCCCTCATCCACCTGCCCAGTGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGC
CAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGTGAAGTGGC
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCCGAGAAG
ACCTGCCCTCCTCACTGGGATCCCCTTCTGCTCCTCCAGGGCTCTGCCAGGGCCTTGCTC
AGTCCCTTCCACCAAAGTCATCTGAACCTCCGTTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA
CTGATGTCTGTCCCCAGGTGCTCTCTCTCCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
TCTCCAGGCTTTATCAAGGTGCTAAGGCCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTC
CGGCCTGGTGTGCTGCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA
GCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTTCTTCTTCC
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG
AGGGAGGCGGCCTCCGCCCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGT
GATCTCTGGTGTCTACAGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCT
GACCAAGTGCCAGGAAGACCTGTGCTATAAACACCCCTGCCTGATCCTGCCCTGCCTGACCC
CGCCACGCCCTGCCGTCCAGCATGATTAAAGATGCTGTCTCTTGGAAAAA

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FIGURE 62

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQGEPPQGSKGDKGEMGSPGAPCQKRFFA
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH
IMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH
LIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

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FIGURE 63

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCACCA
TGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG
ATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTAC
TGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTTACAGCTGCTTCGTGGAAGA
CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAACTGGGTTTCC
CAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTCCGGGAGGAGT
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAAGTGCACAGCCTGTGGTCATAGAA
GGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG
CCAGCCTTCAGTTCAGGGCTACCACCTGTGCGGGGGCTCTGTATCACGCCCCCTGTGGATCA
TCACTGCTGCACACTGTGTTTATGACTTGACCTCCCCAAGTCATGGACCATCCAGGTGGGTC
TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAGATTGTCTACCACAGCA
AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGCCACTCACGT
TCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGAAGTTCCCCGATGGAAAAG
TGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCCTGTCTGAACC
ACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA
GCGGGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTCACCTCCTTCCTGGACT
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAAGAGGAAGGGGACAAGTAGCCACCT
GAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCTGGACTCCCGTGTAGGAACCTGCACA
CGAGCAGACACCCTTGAGCTCTGAGTTCCGGCACCAGTAGCAGGCCCGAAAGAGGCACCCTT
CCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTTGTTTTTTGTTTTTTTGGAGTGGAGTCT
CGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC
TGGTTCAGCGATTCTCTTGCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA
CACCCAATAATTTTTGTATTTTAGTAGAGACAGGGTTTACCATGTTGGCCAGGCTGCTCT
CAAACCCCTGACCTCAAATGATGTGCCTGCTTCAGCCTCCACAGTGCTGGGATTACAGGCAT
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAGAGAGCAGCAAC
TTGCAAGGGCGGCCTTTCCCACTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA
CCCACCCTTTCTACTTCCAAGACTTATTTTACATGTGGGGAGGTAAATCTAGGAATGACTCG
TTTAAGGCCTATTTTCATGATTTCTTTGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGA
TTCCAAATAATATGTTTCCTTCCCTCATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAAT
CAAAATCATCCACTGAAA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWK
TMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKV TALHHSVY
VREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI
ITAACHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT
FNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSF GIGCAEVNKP G VYTRVTSFLD
WIHEQMERDLKT
```

Signal Peptide:
amino acids 1-20

Transmembrane domain:
amino acids 240-284

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FIGURE 65

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCACCCGTTAAGGTGTCTTCTCTTTAGGGATGGT
GAGGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG
AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC
ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC
AGGAGGACTTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCA
TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC
TTTTTACTAGCAAAAGTGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG
CCCATCATTTTCATTCATCCTTGCCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGCAGCACTT
ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTTCCCTCCTGAATCCGAAGCAGGATCTGAA
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTTGTTA
AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTG
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTTGAACAGCTAATAAAGATTT
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA
TAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATCAAAGACTTAATATATTGAAGTAACACTT
TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTCACAGAATGGAATTTTTTTGTTTCATGTCT
CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTTAACTCATGCACA
TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTA
TTTTCTTGTGTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG
AATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTTTATCATGAAATCATGTTT
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC
ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAATAAATTAAAA

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FIGURE 66

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLEFVTFDL
LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQEAEEENRLLIV
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL"

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

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FIGURE 67

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC
CAACCATTCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGACT
AACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC
GGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGC
CACCTCAACGTCCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGCTACAC
AGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGAACAACCTGCTCTGAGGA
GATGTTCCCTCCAGTTCGCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGT
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCTGATGCTGAGAAACGTGCAGCCGGA
GGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA
GATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGACCGGGACTCCACGGTGGCCGTGATTGT
GGGTGCCTCCGTGCGGGGCTTCTTGGCTGTGGTTCATCTTGGTGCTGATGGTGGTCAAGTGTGT
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG
TGTCCTCGTCTCTCCCTCTCCGCCCCTGTACAGTGACCTGCCTGCTCGCTCTTGGTGTGCTT
CCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCGACTTCGTATCTCCCA
CCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGGAGGCAGGAGGCAC
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGCTGTCACC
TGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCCTGT
GCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTGTGCTCCTCCCTGCTCCAG
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGAACTTGGAGGGGCATGTTAAA
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT
GCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC
TGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG
GGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG
AGGGGTGGGGCTCCATGGTGAATGCAGGTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA
CCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG
CTTTCTTTGGGGCTTCAGTGAGAACTCTCCCAGTTGCCCTTGGTGGGGTTTCCACCTGGCTTT
TGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGGAACTGAGCT
GCCAATGCCAGCCCTGTCCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACTCCCTTC
GTGGGGACAAAAGTGACAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCAGCACTT
TGGGAGGCCAAGCGGGTGGATTACCTCCATCTGTTTAGTAGAAATGGGCAAAACCCATCTC
TACTAAAAATACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCAGCTATTTGGGA
GGCTGAGGCAGGAGAATCGCTTGAGCCCCGGAAGCAGAGGTTGCAGTGAAGTGAATAGTATGAT
AGTGCCACTGCAATTACAGCTGGGTGACATAGAGAGACTCCATCTCAAAAAAA

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FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQF
SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGIYN
CYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQ
KLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

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FIGURE 69

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCCGCCCGCAGCCTC
GTTTCGTGTCCCCGCCCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
GCAGCTCCCTTCCCACCCCACTGCAGGTCTAATTTTGGACGCTTTCCTGCCATTTCTTCCAGGTTGAGGGAGC
CGCAGAGCGGAGGCTCGCGTATTCTGCAGTCAGCACCCACGTCGCCCCCGACGCTCGGTGCTCAGGCCCTTC
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGCCGTCCGGTTTGGCT
CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
ATCCTGAGGTCATTCATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGTCTCATGGCTAGA
GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGTCTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCGGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAAGACTTT
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA
CAGGTGCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGCAG
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA
CATGGGCGGCCCCTGTTCTGCTTGCCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
CATGTCCGACAAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTTGTTCT
TGTGAAGTAAGATTAAGAGATCAGTGCAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCT
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC
AGAGTGTGTTGCTGTTGTGTAAGTGAATACTTGAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAAGGTGCCAAATGCATA
TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTGTAGAAATCCTGTGTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTGTCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACCTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
CAAATGAATCTGTTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
ATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATCTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGTATATAA
ATATTGCCATATCATGGTACCTATAATGGTGTATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
AATCTGTAAATGTTAGTTTTTGGTAATTTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGA
TAAACATTAAAAATTAATCATGTTTCAAAAAAAAAAAAAA

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FIGURE 70

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLLEKYMDEDEGEWWIAKQRGKRAITDNDMQ
SILDHLNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPIYEHCNPYCPFRCSGPVCTHYTQVWATSNRIGCAINLCHNM
NIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRYYP
EEETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRVFAVV

Important features:**Signal peptide:**

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

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FIGURE 71

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC
TGGGCGCGCCCCCGGGCCCCGCCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCT
CTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCC
CTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCC
GAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCGCGGGCGCC
GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTACCTGGAG
ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT
GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA
TACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT
GGGGAAGACCTCGTCAACATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACT
ATTTTTGAATCAGAGAATTTCTTTTTGCGCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA
GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT
GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC
TGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATCTGAAATTGGAAATTGGA
GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC
ACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGAAGCTGTGGCCCGCGCA
TCTCTGATTCCAGAATTCTCTGATGGTTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAAT
TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC
AGGTCAATTCGATATCACAATCCTGCCTCAGCTTTACATTACAGCCCATGATGGGGGCCGGCCTG
AATTATGAATGTTACCGATTTCGGCATTTCCCCATCCACAAATGCGCTGGTGATCGGTGCCACG
GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC
CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGAT
GTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTAT
GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT
CGGTGTCAGCGTCGCCCCCGTGACCCTGAGGTGCTCAATGATGAGTCCTCTCTGGTCAGACAT
CGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA
CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGCTTCAAT
CTCTGTTCTGCTCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTT
CAAATCCTCCCTACTTCCAAGAAAAATAATTAACAAAAAACTTCATTCTAA

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGLALA
LEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI
DTYFDTERSSTYRSKGFDTVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFLLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSGTTLLRLPQKV
FDAVVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAIEIAGAAV
SEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLLLPFRCQRRPRDPE
VVNDESSLVRHRWK
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

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FIGURE 73

CGCGCGGCGAGAGCGCGCCAGCCCCGCCGCGATGCGCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCCGGGCCAGG
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACC
TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTGATGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGGCAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAAGTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGGAAACCGCCAGTGCCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCCTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTGCTCCGGAACACAGGTTCTGTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
TGGAGTCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG
CTGAGCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA
TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA
AAAAGGAATCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTCAC
CTCTCCTGCCAGCTCCCGCACCTGCGTTTAGGAGTTCAGTCCCACAGAGGCCACTGGGTTCCCACTGGTGGCT
GTTCAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAG
ATTCTTTATTAAAGTTAAGTTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAACATTTTCAGTGGCGATA
TATCCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC
TGGAGCTTCFGTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTCGATACTTGTCAAATCAGTTACTGTTCAAGGGAT
CCTTCTGTTTTCTCACGGGGTGAAACATGTCTTTAGTTCCCTCATGTTAACACGAAGCCAGAGCCACATGAAGTGT
TGGATGTCTTCCCTAGAAAGGGTAGGCATGGAATTTCCACGAGGCTCATCTCAGTATCTCATTAACCTCATTGA
AAGATTCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTTCTGTTTTCTCAGTAGTCCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAAGTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
CTGCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG
TATGGTTTACAGATAATTCTTTTTTTAAAAAAACCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACCTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTACACATAT
GATACTTTCTAAATAAACTCTTTTTTTTTAA

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FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHSK
HLYTADMFTHG IQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAHS
VCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPELKQ
GLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQHYE
LCSGNQVRGYPTLLWFRDGGKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:
amino acids 1-32

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FIGURE 75A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACACGCAAGACCAAGCGGGCTCCGCGCGGACCGGCGCGGGGC
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCC GCCCGCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGGTGTGTTTTTTCTCCAGAGAATTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAATGTGC
TGGAGAAGAGCGACCCCTCCTTGTCTTCCGGAGTCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTGTGTTGGGTGCATG
TGTGCGCCCGCAGCGGGCGGGGCGGTGTTCTCCGCTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTGCGGGGCATCCGCTCCGCTTCTCCAGGCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG
CGCTGGCAGGATTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCTTAGAAGAGGAGG
AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACTTCCACCTCCCAGCCCCATCTCA
TTTTCATCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTACCACGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGTGGCAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAAGTATCAGATACACACGGACTTCAACATTCTATCATAGACCTACCCACCCCACTGTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGAATGCATGCCACCAGAAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCCAT
ACCCACAAAGCCTATATTTTTATATACTGCCATCAAGCTGTTTCATTACCACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATGGGAAGGAGGGATCC
GGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGGTGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACC
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGATTCAACAAAAC
TGCAGTGCCGGTCAAGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAACCAAGAAAAGAAGCCAAAGCAAAATCAGGCTGAGAAAAGCAAAAGAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAAGTGTCTGCTCAGTG
CCAAGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCTGAGTTCCACTGCTGTGCTTCAGTCAACTGACCAACACTGCTTTGAATTATAGGAGGAGAACAATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC
AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTCTTGGTGAATTTTGTATGTCTGTATATGA
CACTTGGGTTTTTAAATTAATCTATTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAATTTTCTAAACACTTTACTAGAAGAACATTTCACTATAAAAAACCTAATTTATTTTACA
GAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTCTGCTACCATTAAGAAGA
ATTTTATTTCAATTTCTTCAAATTTCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTACAGAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
AATTATTAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAT
GTATCATTGGTCTTAAAAATAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACCAACCACAGTAA
TATATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCATAATAATAACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCGCTGGAGTAGGTAACCTTGTGGAACCC
ACATGCAACGTCATGAGGAGAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCCTGGTGTCTTTCTTGAAGTGCCCTCTCCTAATGCAGAGGCTTGAAGCTTAC

FIGURE 75B

AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAAATTTACTAAATTGGGTAAGATGATTTAAATGATTTTAATTTTAAACATTTTATTTCTAGAATATAT
GGCTCACTTTTATTTTATAGTGTAAAGTTGTATTTTCTTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTGTTCTATGTTTAAAAAATAAAGGAAAAAATAAAGGAAAAAATAAAGGAAAAA
AAAAAATAAAGGAAAAAATAAAGGAAAAAATAAAGGAAAAAATAAAGGAAAAAATAAAGGAAAAAATAAAGGAAAAA

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FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFQDVGYHGSEIKTPTLDKLAAGVKLENYYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKECMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYEN
DNAAWDYDNGIYSTQMYTQRVQQILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGFVHSPLLKNKGTVCHEL
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFSTSQPTHMRGWYLTGIQES
```

Important Features:**Signal Peptide:**

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 77

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTTCACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTCACTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCAGAGGTAGGACGCGAGCTTTTCGCCCT
GAATCCGCGCAGCGCGAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGGCCATCAAGTG
TCAATTAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTTCGTGAAAGTGAATTAGAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGCTAGTAAGTACCCGAATTGGTGTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCTCCGACGGGGCGGACCCGGTGGCGACAGGCACCCGCGG
CATCCGCGTGATGGTCTGGATGCGAACGACAACGCACCAGCGTTTGTCTAGCCCGAGTACCGCGCGAGCGTTCC
GGAGAATCTGGCCTTGGGACACGCGAGCTGCTTGTAGTCAACGCTACCGACCCCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCCTCCGGTATGTGGACGACAAGGCGGCCAAGTTTCAAAGTAGATTGTAATTCAGGGACATATC
AACAATAGGGGAGTTGGACCACGAGGAGTCAAGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGAGCTGAACGACAATGCCCGAGAAGTGGTCTCACCCTCTCT
CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTATCCACGAAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGGCTCTT
CCCTCAGGCCTCTATTCCGCTTATATCCCAGAGAACAAATCCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
CGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCCCTCAGCAGCAACGTGTCTGAGCCTGTTCTGT
GCTGGACCAGAACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCGACGGACGGTCCACTGGCGTGGAGCT
GGCTCCCCGCTCCGACAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCAAGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCGGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGCGAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCTCGCCTTCGTCTCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAAGTCAAGCCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTCGCACTTTGTGGGCGTGGACGGGGTGCAGGCTTTCTGCGAGAC
CTATTTCCACGAGGTTTCCCTCACCACGGAAGTCTCGCGGAAGAGTCACTGATCTTCCCCAGCCCAACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTCTGTCAGGTGATTGCGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTAAATTGCTCTGTCTCCCAAGC
TGGAGTGACGCGGTACGATCATAGCTCACTGCGGCTCAAACCTCTAGGCTCAAGCAATTATCCACCTTTGCGT
CCGGTGTAAACAGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCAGCCTGTAATCCAGTACTTTGGGAGGC
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGGAGCCAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA
AAAAATACAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AAACTCTATCTCA

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGLTWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVDQD
SEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAYIPENNPRGVSLSVSTAHDPCDCEENAQITYSLAENTIQQASLSSYVSINSDTGVLIALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSI PQVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVDGVQAF L
QTYSEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNC SVS
QAGVQRYDHSSLRFPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLW
EAEAGGSPEVGSLRPA
```

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

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FIGURE 79

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTGCTGCGCCTCCTC
GTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTGTCGTTGGGAGCATCTCA
GAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTC
ATGGACTCGGTGCGCCGCGGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAAACGGCGCTGGAAC
TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTGTAC
GCCATCTCTTCGGCAGGTGTGGCCTTTGCAAGTGACGCGGGCGTGCAGCAGTGGGGAGCTGGAGAAGTGCGGCTGT
GACAGGACAGTGTCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG
GCCTTCTCACAGTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC
CACAACAATGAGGCCCGCAGGAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGGC
TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAGAAGTTT
GATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAAG
CCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG
CTGGGCACGAGGGGCGCACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC
GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCTACTGGTGTCTTTCGTCAAGTGC
CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGAACCGCCTGCCTAGCCCTGCGCCGGCAACCACCTA
GTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCCACTACCCCAAGAGATACTGGTTGTATTTTTTGT
CTGGTTTGGTTTTTGGTCTCATGTTATTTATTGCGGAAACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGC
CTCCCCAAAGCCTGGGCCTTTGTGGCTGCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTG
GCTGCCACTGACCACTCAGTTGTATCTGTGTCCGTTTTTCTACTTGACAGCCTAAGGTGGAGTAACAAGGAGTA
TTACCACCACATGGCTACTGACCGTGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATAGGTACCGACTTG
ATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAAGTCTCCAGCACACATACACATGGACTCCTGGCAGCTTGA
GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTTATT
TCAGCCCTTACATGGACAGCTAGAGGTTGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG
AGACGACTGAAGTCCACCCCTAGAAGCCAGCCTGCCCCAGCCTGCCCCGAGGAAAGAGGAACTTAACCACTCCCC
AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCGA
GTCACCTTTCACAGCGCTGTTCTCCATGAACTGAAAAACACACACACACACACACACACACACACACACACAC
ACACACACACGACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAG
TCACCTTTCACAGCACTGTTCTC

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FIGURE 80

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRRWNCSTLDSLPGKVVTOGTREAAFYAIAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGSDNIAYGVAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCRAVP
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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FIGURE 81

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCTGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAATCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAGAGAAATCATGCCCGACCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCC
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCA
AAACAAAGCGACAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTGAACTCCTTGCCCTCTTACCCAAATCACC
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGTGTGAGGGATA
TCTATCTAAAGAAACACAAACTCCTGCCCAATGATTGGTCTGCAGACAGCTCTATTTAGAGACCACTGGGAAAA
GCCGGACCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGCCTGTCTGCTCTGGAGCTGCTATTGCCCGGTAAAGAACAGTATCTGGAAGAGGAGC
AGCGTCGTGAGTACCTCCTACGTTTGAAGAACAGCCAGCTGGAGAAAGACCTACGGGGAGATGGCCAGATCGTGG
ATGTCCCCCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGT
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAGAAGAAATTGACTTCGGGTATTCTCTCTGGGTGCCACCCCATCCTGAACCAAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAGCTCTTGGCCCTCTACTCTGCTCATGATGTCAGTCTGT
CACCAGTTCTCAGTGCCTTGGGCTTTTCAAGAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT
CTTTCTGCCAAGACCACCAAGCGTTCTCCCAAGCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTCTAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAATTTTTTTAATCTTAGACATT
TTTACCTGTCTTGTGTTAAGAAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTCTGTAAAGG
GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTACATACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAGGAATATGTGTAGCTGGGTCCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACTTCTGCTAGAAACA
CAGAAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTAAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTGTATGCCATTTAGTATTTTATAGTTTAGGAAAATATT
TTCTAAGACAGTTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACCTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
ACTGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAATGCGTTTTTGG
AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAATAATGGTGCTAATTCAGAGAAATGGAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC
AACTTTTCTCTTTGTTTTGTCCAGTGTGCAATTTGAATATGTCTGTTCTATAAATAAATTTTTTAAGAATAA

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FIGURE 82

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLAALLAFVLSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVPVTEPPVTDPVYEALLYCNIPSVAE
RSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYPHPKLEAFISHMSKSGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLKKHKLLPNDWSADQLYLETTGKSRTLQSGIALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSFPCRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFTTSFCQDHHKRSPPKPMCPLE
NLVRFVKRDMFVALGGSGTNYDACHREGF
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Signal sequence:
amino acids 1-18

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FIGURE 83

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT
GACGTTGTGGAGATGGGGAGCGTCTCGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAGTATGATCTATGCACTTTTCTTG
CTTGTTGGAGTATGTGTAGCTTGTGTAAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTTGGATTT
TGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGT
TTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTG
CACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCAGAAAGGA
ACTTTTACAACCTGTGTGTTTATGTAGGCATGGCAGGTGCCCTTTGTTTCATCCTCATACAACCTAGTCTTACTT
ATTGATTTTGCACATTGATGAATGAAATCGTGGGTTGAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCA
GCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTACTACACT
CATCCAGCCAGTTGTTTCAAGAAACAAGGCGTTTATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG
TCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTTTGTACAGTCTTCAGTAATTACAGTCTACACA
ATGTATTTGACATGGTCACTATGACCAATGAACCAGAAACAATTCGAACCCAGTCTACTAAGCATAATTGGC
TACAATACAACAAGCACTGTCCCAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTA
ATTTCTTTTTTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAACTGACTCTA
ACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGATCACTGGAGGATGGGGACGATGTT
CACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCCTTCTTTCACTTCATGCTTTTCTGGCT
TCACTTTATATCATGATGACCTTACCAACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGTCAGTGGACA
GCTGTCTGGGTGAAAATCTCTTCCAGTTGGATTGGCATCGTGTGTATGTTGGACACTCGTGGCACCACCTTGT
CTTACAAATCGTGATTTTGAAGTGAAGTGTGAGACTTCTAGCATGAAAGTCCCCTTTGATTATTGCTTATTTGAAAAC
AGTATTTCCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATGTAACTTCTCCAGTGTTCTGGCATGAATTA
GATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAAGTGCATTGATATGTGAAGTAGAATGAATGCAGAGGAA
AGTTTTATGAATATGGTGATGAGTTAGTAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAT
GAAGAGTAAAAACAATTTGTTTGAAGTATTTTAAATTTATATAGACCTTAAGCTGTTTTAGCAAGCATTAAAGC
AAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATACCTGCAAGAACATGGTTTATTTTAA
ATTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTACCCTTGATACGGAATTTACA
CAGGTAGGGAGTGTTAGTGGACAATAGTGTAGGTTATGGATGGAGGTGTGCGTACTAAATTTGAATAACGAGTAA
ATAATCTTACTTGGGTAGAGATGGCCTTTGCCAACAAAGTGAAGTGTGTTTGGTTGTTTTAACTCATGAAGTATG
GGTTCAGTGGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTTAGAAGGAA
GTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCACGACGCTAGCTCACCCTTGGTAATCCAGCACTTTG
GGAGCTTAAAGTGGTAGATTACTTGAGCCAGGAATTCAGACCAGCTTGGCACATGGTGAACCTGTTCTATAAAA
ATAATCTGGCTTTGAGCATATGCCTGTGGTCCAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCAGAGCCAAAG
GTTGCAGTGAGCAAGTCACGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTGAAAT
CAAGGAGGCCAAAATTTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTATATAAAATC
TAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA
ATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAAAAATATTTCTATTCAAAATACATGCATATTGAT
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAACAGGTGAGAAGA
ATGATGGAATGTTTTAGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGT
ATTTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGTATGAGAGTTTA
GTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAAAATCTACAATTTCTTCTTTAAAAATATTTATTAAT
GTGAATGGAATATAACAATTCAGCTTAATCCCAACCTTATTCTGTGTGTAGACATTGTATTCCACAATTTTGA
ATGGCTGTGTTTTACCTCTAAATAAATGAATTCAGAGAAAAA

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FIGURE 84

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTT
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVITYSYSEFFHMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSWIGIVLYVWTLVAPLVLTNRDFD

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FIGURE 85

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT
GTGGCGGTCTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG
AACCGTACAGCTGCAGGGGGAAACCGAGTCCGCCGGGCCCCAGCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGA
ATCTTTTACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCCCC
CGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACCGCCACCATCCCCGCCACGCTCGCTGAGGCTGC
TGTCGCCGGTGCCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTGTTCCCAGGACAAGTGGACCCCATGTTTCC
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGC
ATGCCCCAGTGTACTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG
AGCAAGGGTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATGACAAGC
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCT
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTTGGTTTGGAGAAGGCAGTGTGAGGCTGCACAGT
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 86

MLGLLGSTALVGWITGAAVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPFRRRGHLGIFHHHRH
PGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

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FIGURE 87

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCGCACGCACGCACACACGCGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCCGCGA
CGCCCGCGCCCGGCTCGGCGCCCGCTGGGATGGTGCAGCGCTCGCCGCGCGGCGCCGAGAGCTGCTGCACTGAAG
GCCGGCGACGATGGCAGCGCGCCCGCTGCCCGTGTCCCCGCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT
GCTCGCGCCCTGCGAGGCGCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTTCAGTGCCTCTGT
TCGGAGTGGGGACCTCTGGATCCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT
ACAACGGGAAAGCAAAGAAGTATCATAAATCTGGAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAAATGA
AAGCTATGTCTTAGAACCAATGAAAAGTGCACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACACACCAAACTCGCTGCAAAGAATGTGTTCCACCACCCTCTCAGAC
ATGGGCAAGAAGGCATAAAGAGAGACCCCTCAAGGCAACTAAGTATGTGGAGCTGGTGTGTCGAGACAAACCG
AGAGTTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTCCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTTGTTCAGTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCACTGTCGGGGAAATTGTTCATGGACCATTTCAGACAATCCCTTGGTGCAGCCGTGACCCTGGCACA
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAAGCTGGAGAAAGGAATGGGGGTGTGCTTGAACCTGCCGGAAGTCAGGGAGTCTTTCGGGGGCGCA
GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGAGGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCCTGAAGCCGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTTGCACAGGGGCCAGCCC
TCACTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTTCAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATTTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCCCTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCGGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG
CTGCTGCAGAGGAGGTACGCGCTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
CAGTGCAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAAACATGGACATGCTTCAGTGCTGCTCTCTGAG
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCTTTCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAT
AGCAGGTTTTAGTTTTTAAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAAGTGAATGGCAA
TGAAACAAAGTGGAGAAGAAGGTAGGAGAAAGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGGTTTTGAGGGTTTGAGAAAGCCAGGGAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

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FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDKSNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLAAKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQGDLEKVKQRLIEIANHVDFYRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFPMNHDTLDRGCSCQMAVEKGGC
IMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEECDCEPEECMNRCCNA
TTCTLKPDVAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQDGYCYNGICQT
HEQQCVTLWGPGAKPAPGICFERVNSAGDPYGNCGKVSFSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPLOQGGRIKRGTHVYLGDDMPDPGLVLAGTKCADGKICLNRRQCNISVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDFGFGGSTDSGPIRQAEARQEAAESNRERGGQEPVGSQEHASTASLTLLI
```

Signal peptide:
amino acids 1-28

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FIGURE 89

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGG
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAATGCTCTGGATTTCTA
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCA
TACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTT
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGA
ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA
TGGCAGTGAACACATCTGATTTCCACAGCACACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCC
CAACCTTTTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATC
ACGAGAACACCTAAACAACAACCAAAATCTATTGTGGTATGCACTTGATTAACCTATAAAATGTTAGAGGAAAC
TTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATTTGTA AAAAATAAAAAGAAATTACAAAAGAAATT
ATGGATTTGTCAATGTAAGTATTTGTCTATCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGT
GTTTATTCAAATGTGGTCTCTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCC
GTGGTCAAATTCCTCCTCACTATAATTGGTATTTACTTTTACCAAAATCTGTGAACATGTAATGTAAGTGGC
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG
TGTCCCTTCATGGAAGGTCTCCGCTGTGCCTCTCATTCGAAGGCAGGAAGATGTGACTCAGCCATGACACG
TGGTTCGTGGTGGGATGCACAGTCACTCCACATCCACCACTG

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FIGURE 90

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDAAVIYPTMKDFNHSYHACGVIATIAFLMINAVSN
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG
RTEDLWQ

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FIGURE 91

CGACGCCGGCGTGAATGTGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGCTCCTCTGCAAAGTTA
CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGCCCCCAGCGCCCCTGGTAAC
TGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGCTTTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGT
GGTAATTGGCAGTGGCTTTTGGGGGCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCCTGGTGCT
GGAACAACATACCAAGGCAGGGGGCTGCTGTACATACCTTTGAAAGAATGGCCTTGAATTTGACACAGGAATCCA
TTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTATCTTGGACCAGATCACTGAAGGGCAGCTGGACTG
GGTCCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCAATGGCCGAAAGGAGTACCCCATGTACAG
TGGAGAGAAAGCCTACATTACAGGGCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA
GCTGGTTAAGGTGGTATCCAGTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTGCCCCGTGGTTAGCT
CCTCGACAGTGTGGGCTGCTGACTCGTTTCTCTCCATTCCCTTCAAGCATCCACCCAGAGCCTGGCTGAGGTCCT
GCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCACTTACGGTGTACCCCCAA
CCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTACATGAAAGGAGGCTTTTATCCCCGAGGGGGTTC
CAGTGAAATTGCCTTCCACACCATCCCTGTGATTGAGCGGGCTGGGGGCGCTGTCTCACAAAGGCCACTGTGCA
GAGTGTGTTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTA
TTGCCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGCCGCTGCCT
GCCAGGTGTGAAGCAGCAACTGGGGACGGTGGCGCCGGCTTAGGCATGACCTCTGTTTTCATCTGCCTGGCAGG
CACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTATGTTTACTATGACACGGACATGGACACAGGCGATGGA
GCGCTACGTCTCCATGCCCAGGGAAGAGGCTGCGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATCAGCCAA
AGATCCGACCTGGGAGGACCGATTCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTT
TGAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGACTATGAGACCTTCAAAAACCTTTTGTGGAGC
CTCTATGTGAGTGGTCTGAACTGTTCACACAGCTGGAGGGGAAGGTGGAGAGTGTGACTGCAGGATCCCCACT
CACCAACCAGTTCTATCTGGCTGCTCCCCGAGGTGCTGCTACGGGGCTGACCATGACCTGGGCCGCTGCACCC
TTGTGTGATGGCCTCCTTGAGGGCCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTG
TGGACTGGTGGGGGCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGACCT
TAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAATTAGTTCCATCAGGGAGGAGTCAGAGGAATTTG
CCCAATGGCTGGGGCATCTCCCTTGACTTACCATAATGTCTTCTGCATTAGTTCCTTGACGTATAAAGCACT
CTAATTTGGTTCTGATGCCTGAAGAGAGGCGCTAGTTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGC
TTCCAGCTGGGGCAGGTGAGATCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATA
GCTTGATGTCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGAATATT
CCATCTGTGGATAGAACCCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTTCACTTCTGCTCCTGAGGCTTCTGCT
CTCATTCATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGGGAAAAGGGAGACTAATGAGGCTTAATCAAAA
ACCTGGGGCGTGGTTTTGGTTGCCATTCCATAGGTTTGGAGAGCTTAGATCTCTTTTGTGCTGGGTTCACTGGCT
CTTCAGGGGACAGGAATGCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT
TAGTAGGCTGCATGTGATGATCATATCCAATTATATGGAAGTCCCGGGTCTGTCTTCTTATCATCGGGGTG
GCAGCTGCTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGCCTTATCCACCAATACACAGG
GAAGGGTGTGAGGGAAGGGTGACATCAGGAGTCAAGGGCATGACTGGTAAGATGAATACTTTGCTGGGCTGAA
GCAGGCTGCAGGGCATTCCAGCCAAGGGCACAGCAGGGACAGTGCAGGGAGGTGTGGGGTAAGGAGGGGAAGTC
ACATCAGAAAAGGGAAAGCCACGGAATGTGTGGAAGCCAGAAAATGGCATTGTGAGTTAATTAGCACATGTGAG
GGTTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTGGTATCAGACAT
ACGAAAGGTCTCTTTGTAGTTCTGTGTTAATGTAACATTAATAAATTTATTGATTCCATTGCTTTAAAAA

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FIGURE 92

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVTVVIGS
GFGGLAAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS
SPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQEEAIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRC
GLLTRFSFPLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHMKGGFYPRGGSSEIA
FHTIPVIQRAGGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLPGVK
QQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYDMDQAMERYVSMPREEAAEHIPLLFFAFPSAKDPTW
EDRFPGRSTMIMLIPTAYEWFEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLFPPQLEGKVESVTAGSPLTNQF
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPINLYLTGQDIFTCLVGLALQGALLCSSAILKRNLYSDLKNLD
SRIRAQKKKN

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FIGURE 93

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGTGCGGCTCGGGATGG
GTCCAGGATGTTACTCCTTCTTCTTTTGGTGGGCTCTGGGCAGGGGCCACAGCAAGTCGGGGCGGGTCAAACGTT
CGAGTACTTGAAACGGGAGCACTCGCTGTGCAAGCCCTACCAGGGTGTGGGCACAGGCAGTTTCTCAGTGTGGAA
TCTGATGGGCAATGCCATGGTGTGATGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTT
GTGGAACCGGGTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAAGAA
GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTTGGAAACAT
GGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC
CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGGCGGCTACAGAGCTGGG
AGGCTGCACAGCCATTGTCCGCAATCTTCATTACGACACCTTCTGGTGATTGCTACGTAAGAGGCATTGTGAC
GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCCCCGCGG
CTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCAATTCCTTGAAGTTGTTGA
ACTGACAGTGGAGAGAACCACCCAGAGAGGAAAAGCTCCATCGAGATGTGTTCTTGCCCTCAGTGGACAATATGAA
GCTGCCTGAGATGACAGCTCCACTGCCGCCCCGTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGT
GTTTTCTGTATTTGCCATAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTCTA
CTGAGCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTGGCCTGAGCA
TGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTGAATGCAGG
GACCCCGCATTCCCATGGTGTGTCATGGGGACATCTAATCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT
GCTGTGATGTGCCTTTCCCTGCAGTCCTTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGC
CAAAATCACAGAACAGAATTTATAGCCCAGGCTGCCGTGTTGTTGACTCAGAAGGCCCTTCTACTTCAGTTTT
GAATCCACAAAGAATTAATACTGGTAACACCACAGGCTTTCTGACCATCCATTGCGTTGGGTTTTGCATTTGACC
CAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAAACTTCTTCCCTGCCTTACCTTCTTTCA
CTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGG
CTGCAGAACACACCTGCCCTTCACTGGCCTTCAATAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG
TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTACAGGCCCTCAGTGAA
GTTTGGCTAAAGGTTGGTGTAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC
TGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTGATGTGGTCTGACCATGTGGAGATGTTTCTGGAC
TTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGTTACGATTTTGGAAATCCACTTTGAGTGCTGAAAGTGAAG
GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAA
GAGACAGTTGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTTCACTG
TCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCTTATTCCACTGCCTTATTGACAAGGGGTTACAT
GCTGCTCACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCCTGGAACCTGAGTC
CTCCTATGAACCTCTGTAGCCTAAATGAAATTTCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCG
GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

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FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFQKHGQKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTLGGCTAIVRNLYDTFLVIRYVKRHLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFYTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLP
EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQRKRFY
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Signal sequence:
amino acids 1-38

Transmembrane domain:
amino acids 310-329

FIGURE 95

CTTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA
 ACCTCGAGCTCACACCAACAGACACACGCGGCATACACACTCGCTCTCGCTTGTCCATCTCCCTCCCGGGGAG
 CCGCGCGCGCTCCCACCTTGGCCGACACTCCGGCGAGCCGAGCCCGCAGCGCTCCAGGATTCTCGGGCTCGGA
 ACTCGGATTGACGCTCTGAACCCCCATGGTGGTTTTTTTAAACACTTCTTTTCTCTCTTCTCCTCGTTTGATTGC
 ACCTTTTCATCTGGGGGCTAGAGGAGCAAGGCAGACGCTTCCAGCCAGCCCTTGTGGCTTGCCATCGTCCA
 TCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTCGCTGCTCGTCCCTCGGCTGGCAGAAGGGGTG
 ACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTTTGGCTTGGAGGGGCAAGGTGAAGAGCGCAC
 CGGCCGTGGGGTTTTACCGAGCTGGATTGTATGTTGCACCAATGCCTTCTTGGATCGGGGCTGTGATTCTTCCCCT
 CTTGGGGCTGCTGCTCTCCCTCCCCCGCGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCGAGGCGTA
 CGTGCCAAGGGATTACGCTTGGCGGACATCCCCTACCGAGGATCGCAGGGGACACTTAAAGATCTGCTCTCA
 GGAATATACATGCTGCACACAGAAATGGAAGACAAGTTAAGCCAAACAAAGCAAACTCGAATTTGAAACCTTGT
 GGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGGCATAAGAAATTTGACGAATTTTTCGAGAGCT
 CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGA
 AGTCTTTCAGGACCTCTTCCACAGAGCTGAAAGGTTACTACATGGGGGTAATGTGAATCTGGAGGAAATGCTCAA
 TGACTTTTGGGCTCGGCTCTGGAACGGATGTTTCAGTGTATAACCTCAGTACTCACTTGAAGACTACCT
 GGAATGTGTGAGCAATACACTGACCGATCGAAGCCATTGTGAGACGCTGCCCGGAACTGAAGATTAGGTTAC
 CCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA
 GGTGAGCCCAACCCAGGCTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCATACTGTGGGGGCTTCCCAC
 TGTGAGGCCCTGCAACAACTACTGTCTCAACGTCATGAAGGCTGCTTGGCAAACTCAGGCTGACCTCGACACAGA
 TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCAGTGGAGGGGCCATTCAACATTGAGTCGGTCA
 GGACCCGATAGATGTCAAGATTTCTGAAGCATTATGAACATGCAAGAAAACAGCATCGAGGTGCTGCAAAGGT
 CTTTCAGGGATGTGGTCAGCCCAACCTGCTCCAGCCCTCAGATCTGCCCGCTCAGCTCCTGAAATTTTAATAC
 ACGTTTCAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGA
 CATAAAAGAGAAATGAAGCTCTCTAAAAGGCTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGCGT
 GCAGCGGGCAGCTCCAACGAGGAGGAATGCTGGAAGCGGCACAGCAAGCCAGATCTGCTGAGATCATGAA
 TGATGGGCTCACCAACCAGATCAACAATCCGAGGTGGATGTGGACATCACTCGGCTGACACTTTTCATCAGACA
 GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGA
 CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGGATGACCTGTGTCCCACGGAGTTTGAGTT
 TGTCAACCAAGAGGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCACGCGTGGCCACTC
 CTGCTCTCTGGTCTCTACCTGCAATTGCTCTGGCATGAGAGTGTGCAGATTACTTTGGTTTGGTTCAT
 GATGAAACTGCATTTTAGCTATCTGAATGGCCAACCTCACTTCTTTTCTTACACTTTGGACAATGGACCATGCCA
 CAAAACTTACCGTTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCTCCCTTTTTGTTTTCCCAAAGAGTACC
 GGGTGCCAGAGCTGAATGCTTCTCTCTTCCCTTACGCTATCTGTGGGGACCTTGTATTCTAGAGAGAATTCTTA
 CTCAAATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAATCTCAGGTT
 GTGAGGGTTTTTTTTCTCATTTTAAAT

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FIGURE 96

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENA EKSLNDMFVRTYGM LYMQNSEVFQDLFT ELKRY Y
TGGNVNLEEMLNDFWARLLERM FQLINPQYH FSEDYLECVSKYTDQLKPF GDVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDT EWNLFIDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNMQENS MQVSAKV FQCGQPKPAPALRSARSAPENFNTFRFPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPT EFEFVTT EAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:
amino acids 1-23

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FIGURE 97

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGATATTGACAACTG
AAGCTTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAA
TGGGAAGGTTTTATTGAAAACACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG
CAGAAATTTTATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTTCAT
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT
TCATTACCGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCCTCATGATAATGGCAGCCA
GTTTTTCTTCACACTGGGTGAGCAGATGAACCTTAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATAC
AGTATATAACATGTTGCGACTGTCAGAACTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA
AAGCTGTGAGGTTTTGTTTAACTCTTTGATGACATCATCCAAGGGAATTTAAAGGCTGAAAAAGAGAAACC
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTTACTTTTCATTTGGAGAGGAAGCTGA
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAGCAAAGTAGTCATGACTTGCTTAA
GGATGATCCACATCTCAGTTCTGTCCAGTTGTAGAAAGTGAAAAGGTGATGCACCAGATTTAGTTGATGATGG
AGAAGATGAAAGTGACAGAGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAA
AAAATTAAGGAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG
CAGTGAAGAGCTCAGAAAAGCAAGACAATTAACCGGGAACCTTAGCAGCAAAACAAAAAAGTAGAAAA
TGCAGCAAAACAAGCAGAAAAAAGAGTGAAGAGGAAGAAGCCCTCCAGATGGTGCTGTTGCCGAATACAGAAG
AGAAAAGCAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACCTCCCGGAAGATCAGACCCTTGC
ACTGCTGAACCAAGTTTAAATCTAACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGA
AGTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAGATGCAAG
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAGGAGGGAAGAAAGCAA
AAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAATGAGAATAATGATAACCAGAACCTTGCTGGAAATGTGCCT
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTT
GTCTGGTTTTGAAAAACAATTATCTGTTTTGCAAATGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA
CATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCTTCCACAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFQIQLCLEAYYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESYIGAPFKDEFHSRLRFNRRGLVAMANAGSHDNQSQFFFTLGRADELNNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFNPFDDII PREIKRLKKEKPEEEVKKLKPKGTRNFSLLSFGEEAEEEEEEVNRSQSM
KGKSKSSHDLLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKS
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVAEYRREKQKYEALRKQQS
KKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMShVLQFEDKSRKVKDASMQSDTFEIDPR
NPVKNRRREESKMLREKKERR
```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

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FIGURE 99

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCCACACACACA
ATTTCAACCAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA
CGCATGGGGCCGAAAGGAATTAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG
TTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAATCTACTACATCGTGCAGGAAGAGAAGAAC
TACAGGGAATCCCTAACCCACTGCAGGATTCGGGGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACA
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACCTTCCCTCATCCTACGTATTTGCTATTTTCCTGTGACCGTCATT
CAGTTATTGTTATCCATCCTTTTTTCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAA
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAA

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FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHHTISPGPKGDDGEKGDGPGEKGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGGRYRKFGVQLDISIARLKTSMKFVKNVIA
GIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TPLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:
amino acids 1-25

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FIGURE 101

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC
AGCGGGGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTTCCCTCCGCGGGGGCCAGCCACCTTCGGGAGTCCGGGTT
GCCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCCGAGCGAGTCAATGGCCA
ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCCTTCCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC
CCCAGTGGAGGATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGATGT
CCTGCGTGTGCGCAGAGCACCAGGCGAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC
AAGCAACCCGTGCCTTGATGGTGGTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCCTTGGCATGA
AGTGTATGAAGTGCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGTGCGATATTTCTTC
TTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGA
CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGCTG
GAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG
CACCTTCCAGCGGGAAGACTACGTGTGACCACAGAGGCAAAAGGAGAAAATCATGTTGAAACAAACCGAAAAATGG
ACATTGAGATACTATCATTAAACATTAGGACCTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC
AAACAAACAAACAAAAACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTC
CTCAATATAGGAGGGAAGATTTTCCATTGTATTACTGCTTCCCATTGAGTAATCATACTCAAATGGGGGAAGG
GGTGCTCCTTAAATATATATAGATATGATATATATACATGTTTTCTATTAAAAATAGACAGTAAATACTATTCT
CATTATGTTGATACTAGCATACTTAAATATCTCTAAATAGGTAAATGTATTTAATTCCATATTGATGAAGATG
TTTATTGGTATATTTCTTTTTCTGCTCTATATACATATGTAACAGTCAAATATCATTACTCTTCTTCTATTAGC
TTTGGGTGCCCTTTGCCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATTCTTCATGCGTGCCCTTT
TCATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTATTTGTTTTGTGTT
TCATTGGTCTCTATCTCCTGAATCTAACACATTTCTAGCCTACATTTTAGTTTCTAAAGCCAAGAAGATTTAT
TACAAATCAGAACTTTGGAGGCAAATCTTCTGCATGACCAAGTGATAAATTCCTGTTGACCTTCCCACACAAT
CCCTGTACTCTGACCCATAGCACTCTGTTTGGCTTGAATAATTTGTCCAATTGAGTAGCTGCATGCTGTTCCC
CCAGGTGTTGTAACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACTAC
CTTTTGTTCCTTCCCTTAAATTTGATTTGTTTTCCCAAGTGTAATTATCATGCGTTTTATATCTTCTTAATAAG
GTGTGGTCTGTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATAATCTGGTGACAAATATTCTCTCTGTAGC
TGTAAGCAAGTCACTTAATCTTCTACCTCTTTTTCTATCTGCCAAATTGAGATAATGATACTTAACCAAGTTAG
AAGAGGTAGTGTGAATATTAATTAGTTTATATTACTCTTATTCTTTGAACATGAAGTATGCCTATGTAGTGTCTT
TATTTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACATACCTTCATGTGGTTCAGTGCCTTCT
CCTTCTCTCTCTACCACTATTTCCACTGAACAAAACCTACACACATACCTTCATGTGGTTCAGTGCCTTCTCT
CTCTCTACCACTCTATTTCCACTGAACAAAACCTACGCACATACCTTCATGTGGCTCAGTGCCTTCTCTCTCTA
CCAGTCTATTTCCATTCTTTCAGCTGTGTCTGACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTT
TCCAGTCTGTACAGAATGCTATTTCACTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG
ACCTGGATTGAGTCTTGGTGTATCAATCACCCTCTGTGTTTGAAGCAAGGCATTGGGCTGCTGTAAGCTTATTG
CTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATGTTGTGGGGATCCAGTGAGATA
GAATACATGTAAGTGTGGTTTGTAAATTTAAAGTGCTATACTAAGGGAAAGAAATTGAGGAATTAAGTGCATAC
GTTTTGGTGTGCTTTTCAAATGTTTGAATAAAAAAATGTTAAG

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FIGURE 102

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCVSQSTGQIQCKVFDSLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMTFVNARYEFGQALFTGWAAASLCLLGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYV
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins .

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

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FIGURE 103

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGGCTGATAAGCGAGG
CATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCACAGGCGC
GGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATGTGGAAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC
GCGCGCCGCGCCGCGTGGCTGTGCGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTC
GGGTGGTTTTATAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGATGAA
TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC
TTTCAGCTTGCAAAGCAAATTCAATCCCAGTGGAAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT
GTCCTGTTGTCTTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGAAATGAGATTTTC
AACACATCATTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATGTACCACCTTTCAGTGCTTTTC
TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAAGTGAAGACTTCTTTAAATTGGAA
CGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGTTTTTCAGAGGAAATAAGGTT
AAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTGACTACTTTGCTCCTGGGGTG
AAGTCTATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCA
GGAGACCCTCTCACACCAGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATGCAGAGGCTGTTGGTCTT
CCAAGTATCTGTTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAATGGGTGGCTCAGCACCA
CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAACTTTTCTACA
CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA
GCAGTGAACCCAGACAGATATGTCATTCTGGGAGGTACCCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAG
AGTGGAGCAGCTGTTGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGA
ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTGGTCTACTGAGTGGGCAGAGGAGAATTCA
AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT
GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA
GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCAGGATAAGCAAA
TTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGAATGCTTCAGGCAGAGCACGGTATACTAAA
AATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG
TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCGAGGAGGGATGGTGTGTTGAGCTAGCCAAT
TCCATAGTGCTCCCTTTTGATTGTGAGATTATGCTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATT
TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTT
ACAGAAATTGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAATGATG
AATGATCAACTCATGTTTCTGGAAGAGCATTATTGATCCATTAGGGTTACCAGACAGGCCTTTTTATAGGCAT
GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTTTGAT
ATTGAAAGCAAAGTGGACCCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG
CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA
TGTCACCTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGTTGAATATT
ATATATAA

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FIGURE 104

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLLETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NFTQIPHLAQTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIIINEDGNEIFNTSLFEPPPPG
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVARIYGVFRGNKVKNAQLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQGRNINLNGAGDPLTPGYPANEYAYRRGIAEAVGLPSIPVHPIGYY
DAQKLLLEKMGGSSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTIRYINVIQTLRGAVEPDYVILG
GHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAAEFGLLGSTEWAEENSRLQERGVAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPFSGMPRISKLGSGNDFEVFF
QRLGASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLLTVAQVRGGMVFELANSIVLPFDCRDY
AVVLRKYADKIYISMKHPQEMKTYSVSFDLSFSAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAF
IDPLGLPDRPFYRHHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA
```

Signal sequence:

amino acids 1-40

N-glycosylation sites.amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463,
476-480, 638-642**Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366,
427-433, 529-535, 707-713

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FIGURE 105

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTATGTTGGGAATT
CCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGAAAGTCAAGCAGCCAGTGCGATCTCAT
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC
GGCCAGCTAAGATCTGATTTAGACAATGGAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC
ATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTATCAAAGTT
TCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAA
GGAACATTAGTTATCCAGGTGACAGCAAGTGTGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC
AGCTTACTTCAAGGCCAGCCATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGAT
AGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA
ACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAAGTTTATACCGCTTG
ACTGTCTCTGAATCTGACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT
GCAGAAATGGATTACAGCATTGAAGAGGATGATTGCGAAACATTTGACATTATTACTAATCATGAAACTCAAGAA
GGAATAGTTATATTAAGAAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAAC
CATCATGTTCCCTGAGCAGCTCATGAAGTACCACATGAGGCTTCCACCCTTTTCAAGATCCAGGTGGAAGAT
GTTGATGAGCCTCCTCTTTTCCCTTCCATATTATGTATTTGAAGTTTTTGAAGAAACCCACAGGGATCATT
GTAGGCGTGGTGTCTGCCACAGACCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAGTG
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAAATCAGTGTGTTGTTACAACCTA
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTCGATCCCCTGTATGTGCAAGTTCTTAACATC
AATGATCATGCTCCTGAGTCTCTCAATACTATGAGACTTATGTTTGTGAAATGCAGGCTCTGGTCAGGTAATT
CAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTTACTTTAATCTATCTGTAGAAGAC
ACTAACAATTCAAGTTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTACTAATAGAAGTGGTTTT
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACATGGAATCCCGTCACCTTACAAGTACA
AACACCCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATATTTGGGTTTATTTTT
TTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTTCCCTGAGAAAAGTGAAGATTTTCAAGAGAAATATA
TTCCAATATGATGATGAAGGGGGTGGAGAAGAAGATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACC
ATAATGCGGGAAACGCAAGACTCGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT
GGCCCCGACAGTGCCATATTCAGGAAATTCATTCTGGAAGAGCTCGAAGAAGCTAATACTGATCCGTGTGCCCCCT
CCTTTTGATTCCCTCCAGACCTACGCTTTTGGAGGAACAGGCTCATTAGCTGGATCCCTGAGTCTCCTTAGAATCA
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG
TTTGGTCTGTCAGTGCAGTCAAATAATTAGGGCTTTTTTACCATCAAATTTTTTAAAGTGCTAATGTGTATTCTGA
ACCCAATGGTAGTCTTAAAGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGA
TTTCCCTGGAGTAAATACTCCATGGTTATTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTGGGGAGAAA
TGTAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATGTAGGAAGATATTAAGTAGA
TGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATATCATTATTTACTTAGGAAAGAGTAAAAATACCAA
CGAGAAAATTTAAAGGAGCAAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT
CATATTGACATGAAAATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCATGAAGTATTGTTTCCTTT
ATTAA

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FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHHIGQLRSDLNNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDNEPKFLD
EPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQ
AKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSTIGTIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYY
VFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEHHFYFNLSVEDTNNSSFTIIDNQ
DNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVDCGDSGSTQTCQYQELVLSMGFKTEVIIA
ILICIMIIFGFIFLTGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTTS
AEIRSLYRQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGS LAGSLSSLES AVSDQDES YDYL
NELGPRFKRLACMF GSAVQSNN
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

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FIGURE 107

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATTTGACTCAGAGATT
CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCCCAAATGCTATATCTATTAGGGGGCTC
TCAAGAACAATGGAATATCATCCTGATTTAGAAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT
CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTGGCGCCTCATTGCT
GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCCAGC
CCTTGCTCCTTAATTGGATTATATATGAGAAGAGCTGTTATCTATTAGCATGTCACTAAATTCCTGGGATGGA
AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA
AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTC
TGGGAGGATGGATCAACATTCTCTTAACCTTATTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCA
AATTGTGTATGGATTACGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG
AAGTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA
CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCCACTGTAATCTTAACC
AAGAAATGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAG
TAGATCCTTAGACATGGAATCAGGGCAGCCAAGCTGAGTTTTTATTTTTATTTATTTATTTTTTGTAGATAGG
GTCTCACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC
TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTGGTGTTTTTGTAGAGACTGGGTTTT
GCCATGTTGACCAAGCTGGTCTCTAATCCTGGGCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGA
TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGG
TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGG
TGTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAATATATTTCTGAAT
AGCTAAATGAAGAAATGGGAAAAAATCTCACCACAGTCAGAGCAATTTTATTATTTTCATCAGTATGATCATAA
TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTACTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATC
TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCCCCAGGCTG
GAGTGCAACGGCAGATCTCGGCTCACCGCAACCTCCGCCCTGGGTTCAAGCAATTCCTGCTCAGCCTCC
CAAGTAGCTGGGATTACAGTCAGGCACCACCACCCGGCTAATTTTGTATTTTTTAGTAGAGACAGGGTTTCT
CCATGTCGGTCAGGGTAGTCCCGAATCCTGACCTCAAGTGATCTGCCTGCCTCGGCCTCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTTGATATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAA
GTTTTCTGCTTTTTTAAATACAAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC
TCATTGGAACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTTACCAT
TTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATGTGCTGATTTGTCTTATTT
TTTTCATACTTTCCCACTGGTGCTATTTTTATTCCAAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC
CTCTAATGTTGATTAAATATGTGAAAAGAAATGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT
ATGTTATGTGATTTCAATTAATAAAAAAACTCTTATCAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 108

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYQLHFDSQSNTRIAVVSEKGSAAASPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQLCSVPSYSICEKKFSM

Important features:**Type II transmembrane domain:**

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

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FIGURE 109

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCACA
ATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC
CTACCTACCCGTACGCATACATACATATGTGTATATATATGTAAGTACAGAAAGATCGCAGATCATAAAGCAAG
CTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTTATTTGTCAAGATCCCTGTGCGATTCATGCCCT
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTGGTTTTGGGGACATTATGATTTGTGTAAGACTCAGAT
TTACACGGAAGAAGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATATCTGAA
AGTGAAGTCTGATCCTCCGGATATTACCTGTGGAGACCCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTTGATTTTGAAGGAAG
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAATCACTCTGTCTC
TTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAATGATCCT
GGAGAAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA
CATGGATCCTAAATCCGTGAAGGATTTATCACAGCATAACGGTCTTAGAAATCATTTCACAGAGAAGTACTCAAC
AGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTTCGCGCTTTTGTGGACCTCGCCT
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTTACAGTCACAGACCT
GAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGCAGCTACTTTTACGC
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTGATGACAACAGCAA
ATTGACATGCGAATGTGAGCACAACTACAGGTCCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC
TTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACTGCAATACCTGTATCCCCAGTATTTCCAGTATTGG
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACAACAACGTGCGCTGCCTGTG
CCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG
CCAGGGCGCGCCCCCGCACGGCACCCCCAGCGCTGCTGCTGTGACCACGCTGCTGGGAACCGCCAGCCCCCTGGT
GTTCTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTA
CTAACATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAACTAAGAAGGCCCTAAGTAACTAA
GCCATATTTATCACCCGTGGACAGCAGCATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG
TTGATATTATCACTGCAATCACATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA
AACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGGCCCTAGTAC
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT
TACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTAA
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGTGTAACAGCCCCCTCTAAAAGCGCAAG
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGAGCACACCCACTATACAAGAGTGGCTATA
GGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTTATTTTCTTGAACACTGTAAATATGTAGATT
TTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAATGTATCTAATTCGAATCAGCAAAGACTGACATT
TTATTTTGTCTCTTTCTGTTCTGTTTTGTTTCACTGTGCAGAGATTTCTCTGTAAAGGGCAACGAACGTGCTGGCA
TCAAAGAATATCAGTTTACATATATAACAAGTGAATAAGATTCCACCAAAGGACATTCTAAATGTTTTCTTGT
GCTTTAACTGGAAGATTTAAAGAATAAACTCCTGCATAAACGATTTTCAAGGAAATTTGTATTGCAATTTCTTA
AGATGAAAGGAACAGCCACCAAGCAGTTTCACACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTCAGCTG
ACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACCTTCTGCAAAATATGAGACTATTTCC
ACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 110

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVKLDPPDITCGDP
PETFCAMGNPYMCNNECDASTPELAHPPELMFD FEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI
TFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAFHMDPKSVKDL SQHTVLEI ICTEEYSTGYTTNSKIIHFEI
KDRFALEFAGPRLRNMASLYGQLDTTKKL R DFFVTDLRIRLLRPAVG E I FVDELHLARYFYAISDIKVRGRCKCN
LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGREWSPGSYLP I PKGTANTCIPSISSIGTNVCDNELLHCQN
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLGTASPLVF

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FIGURE 111

GGGTGCCGTACAGTCGCGGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCACCGCGTAGACCGGAC
CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCGACCGGTCCCGCCTTTTGTAAACT
TAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCGGTGACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCCGC
TAAGGAACATGGCGAAGGTGGAGCAGGTCTGAGCCTCGAGCCGACGACGAGCTCAAATTCGAGGTCCCTTCA
CCGATGTTGTACCAACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTACAG
CACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATTAATGTATCTGTGATGT
TACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTTTATGGTTCAGTCTATGTTTGCTCCAAGT
ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGT
TTGAATTGCCAGCAGAGAATGATAAACACATGATGTAGAAATAAATAAAATTATATCCACAAGTGCATCAAAGA
CAGAAACACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAAT
GTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAGGAAGAAGATGGACTGCCGA
TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGCCCCAACTGGGAAGGAAGAAGGCCTTAGCACC
GGCTCTTGGCTCTGGTGGTTTTGTCTTTATCGTTGGTGAATTATTGGGAAGATTGCCTTGATAGAGGTAGCATG
CACAGGATGGTAAATTGGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA
AATTAATGTATGATGACATCTCAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACACAGATACACA
CACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAAGTATTGAGGGGGAAAAAGAATGAT
CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATATTGTAATGTCAATTTAAACATTGGTAGG
CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCTTCCCTCGCCTGTTGGTGCTGGCCCTTGGGGAG
CTGGAGCCCAGCATGCTGGGGAGTGCAGTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCT
GCTTTCCGTGTCTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAGGAA
TTGCACTGTGGCAGCATCAGACGTAATCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGA
AATAAATGGCAGTGCTTTGTCACTTAAAGGGACCAAGCTAAATTTGATTGGTTCATGTAGTGAAGTCAAAGT
TTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTATCTCATGTTTTCTTATTGTACAAAGAGT
ACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT
CTCTGGAGAGTCTGGTCAATGTGGAGGTGGGTTTTATTGGGATGCTGGAGAAGAGTCCAGGAAGTGTGTTTTCT
GGGTCAATAAATAAAGTGTATAGGGAGGGAAATTTCTAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA
TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTAATCACAAGTCCAGCGCCAGGTCC
AAGTCTGAGCCTGACCTCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA
GCGAGGGCACCAGCAGTTGTGGTGGGGAGCAAGGGAAGAGAGAACTCTTACGCGAATCCTTCTAGTACTAGTT
GAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGACTATGTAGCATCTTGAA
AGAAAAATTATAATAAAGCCCCAAATTAAGAAAA

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FIGURE 112

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHELKFRGPFSTDVVTNLKLGNPDRNVCFKVKTTAPRRYCVRPNNGIIDAGASINVSVMLQP
FDYDPNEKSKHKFMVQSMFAPTDTSDEAVWKEAKPEDLMSKLRVCFELPAENDKPHDVEINKIIISTTASKTET
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLL
ALVVLFFIVGVIIGKIAL

Important features:**Transmembrane domain:**

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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FIGURE 113

CCCACGCGTCCGGGTGACCTGGGCGGAGCCCTCCCGGTGGGCTAAGATTGCTGAGGAGGCGGCGGGTAGCTGGCA
GGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTTCTCTTGTGGACCATGTCGGTGATCTT
TTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCCCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTT
TTTGGAAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGGGACTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGG
TTGTGACTTTAGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC
AGCCATGGCCTTCTGCTTCTGGAGACCTGTGGTGGGAATTCACAGCTTCTATGACACTACCTGCATTGGCCT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG
TTCCTCTCAGATGGAGTGCAGCTTGGAAAAAATTCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCT
GGAGGACACAGATGTGGCAAATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCG
AATGGAACCAAGTGACAGCCCTGGGTATCCTCTCCCTCATTCATCAACATCATGTGTGCTGCCCTGAATCTCATTCG
AGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGTTGGACCAAACCTCGTGAGC
CAGCCACCCCTGACCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTCTGCTGCTG
GGGAAATCTCATCAGCAGGGAGCCTGTGAAAAGGGCATGTGAGTGAATCTGGGAATGGCTGGATTCCGAAACA
TCTGCCCATGTGTATTGATGGCAGAGCTGTTGCCACAAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATT
CTATTCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA
GTGTTATTTTCATGAATCATTCATATGATTTGATCCCCAGGATTCATTTTGTTTAATGGGCTTTTCTACTAAAA
GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTTT
ATGTTACACAAGCTTCTTACGGTTTTCTTGTAAACAATAAATATTTGAGTAAATAATGGGTACATTTTAACAAAC
TCAGTAGTACAACCTAAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAT
GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAAAG

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FIGURE 114

MSVIFFACVVRVVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIFSSFGDVACMAICS
CQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKWHFNYVSSSQMECSLEKIQEELKLQPP
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 115

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGCGGGGTGTTTGCAATTGAAACGTGAGCGCGACCCGACCTTAAAG
AGTGGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTGCCTGCCCTTTAAGGGCGGGCGTCC
GGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTC
TGGGTGCTTGGCGGCGCGGCTTCCTCCCCGCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCT
GAGCAGAGTATGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG
TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTCAAGAAGCCT
GCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCTG
GCAATTGCCCTGGGTGCTGTCTGCTGCTCCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGG
AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTG
TCCCTCATCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTC
CTGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTGGGTGGCA
TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCTACCTC
TACTCATGCATCTCCTTCTTGGGGTCTGCTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCC
GTCACTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG
GAGGCAGCCCTGACCCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTGCTACACAGA
CAGGTCCTGGCTCTGCAGACACAGAGGGTCCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG
GGCTACCCCTGGCTATGCTGTGCTTGTGCTGCTGACGGGCCGTGTCTGTGCTCATTGTGGCCATCCACATCCTG
GAGCTGCTCATCGATGAGGCTGCCATGCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG
CTGGGCTCCTTTGGTGCCGTCAATCAGGTTGTACTCATCTTTTACCTAATGGTGTCTCAGTTGTGGGCTTCTAT
AGCTCTCCACTCTTCCGGAGCCTGCGGCCCAGATGGCAGCAGACTGCCATGACGCAGATAATTGGGAACGTGTGTC
TGTCTCCTGTCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGGGCTCACTCGCTTTGACCTGCTGGGT
GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTTCTCTACAACGCAGCCTTTGCAGGCCTCACC
ACACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTG
CCGCTGCCCGTCTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCAGTCACTCCAGCTGGGGGTGGGAAG
GAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA
ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATTGCATAATCTGAGCCAGAGTTTGGGACCA
GGACCTCCTGCTTTTCCATACTTAAGTGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGAT
CCCAAATCTGTTTACACATCAATCTGCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTTGA
TGTGCAATAGGGTGGGGTAGGGGCAGGGAAAGGACTGGGGCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC
CTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG
GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGAAAAAAA

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FIGURE 116

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA
LGAVLLLPFSIISNEVLLSLPRNYYIQWLNGSLIHGLWNLVFLFPNLSLIIFLMPFAYFFTESEGFAGSRKGVLR
VYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFSVTG
KLLVKPRLLLEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYP
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMPQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGIFYSSP
LFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCL
LVKFTTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

FIGURE 117

GAGAACAGGCGCTGTCTCAGGCAGGCGCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCTGCTGTCTCTCGCTCTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGGAGTCACTGATGGTGCCGAGGGCCTGTGCATCTCTGTGCCCTGCTCTTTCTCCTACCCCGACAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGGTTCAAAGCAGTGACTGAGACAAACCAAGGGTGTCTGTGGCCACAACACCAGAGTGCAGAGGTGGAATGAGCACCCGGGGCGGATTCAGCTCACTGGGATCCCGCAAGGGAACTGCTCTTGGTGATCAGAGACGCCGAGTCAAGGATGAGTCAACAGTACTTTCTCGGGTGGAGAGAGGAAGCTATGTGACATATAATTTTCATGAACGATGGGTTCTTTCTAAAAGTAACAGTGCTCAGCTTTCACGCCCAGACCCAGGACCACAACACCGACCTCACCTGCCATGTGGAATTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTTATCAGCATTTACCGTGACAACACGCCAGCGCCTGGAGCCCCAGCCCCAGGGAATGTCCCATACCTGGAAGCCCAAAAAGCCAGTTCCTGCGGCTCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGCTCTGCGACAGACAGTCTCTCGTCCATCCTGTGGGCGCTAGACCCCTGGGGCTGGAGCTGCCCGGGGTGAAGCTGGGGATTCAGGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTGCAGTATCCTCCAGAGAACCTGAGAGTGATGGTTTTCCCAAGCAAACAGGACAGTCTTGAAAACCTTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCCCTGGTCTGTGTACACACAGCAGACGCCCCAGCCAGGCTGAGCTGGACCAGAGGGGACAGGTTCTGAGCCCTCCAGCCCTCAGACCCCGGGTCTTGAGAGTGCCTCGGGTTCAAGTGGACCAAGAGGAGGTTCACTGCCACGCTCGGACGCCACCCACTGGGTCCCAGCAGTCTCTCTCAGCCTCTCGTGCATATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTTCTGGGAATCGGCATCACGGCTCTTCTTTTCTCTGCTGCGCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCAGCATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAGAAAGGCCACACCAAACAGTCTCTCGGACCCCTCCTCCACGAGTCTCCTCCCCAGAAATCAAAGAAGAACCCAGAAAAGCAGTATCAGTTGCCAGTTTCCCAGTAACCCAAATCATCTCACTCAAGCCCAAGAAATCCAGGAGGCAAGAGGAGCTCCATTATGCCACGCTCAACTTCCCAGGCGTCAGACCCAGGCCTGAGGCCCGGATGCCAAGGGCACCAGCGGATTATGCAGAAGTCAAGTTCCAAATCAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGGTAGAGTAAGAGGTTGAAGATAACAGAGTGCAAAGTTTTCTTCTCTCCTCTCTCTCTCTCTTTCTCTCTCTCTCTCTCTTTCTCTCTCTTTAAAAAAACATCTGGCCAGGGCAGCAGTGGCTCACGCCTGTAATCCACACCACTTTGGGAGCTTGAGGTGGCGAGATCGCTGAGGTGGGAGTTGCAGACCGCTGGCCAACTTGGTGAAGCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGCACTGGTGGCAGGCGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAACTACTTGAACCTGGGAGACGGAGGTTGCAGTGAGCCAAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCGAGACTCCATCTCAAAAAAAAATCCTCCAATGGGTTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTAAGGTGGTGATGCTTGAAGCCAGGAGTTGCAGACCGCTGGGCAACATGGTGAACCCCACTCTACAAAAAATACAACATAGCTGGGCTTGGTGTGTGCTGTAGTCCCAGTGTGACAGATTAAACCAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACCTACTGGGCTGCATTTCTCAGACAGTGGAGGCATTCTAAGTCACAGGATGAGACAGGAGGTCGTACAAGATACAGGTCTATAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCAACCAATCCCAACAAACCAAGTTGGCCACGAGAGTGACCTCTGGTGTGCTCACTGCTACACTCCTGACAGCACCATGACAGTTTACAAATGCCATTGGCAACATCAGGAAGTTACCCGATATGTCCCCAAAGGGGAGGAATGAATAATCCACCCCTTGTATTAGCAATAAGCAAGAAATAACATAAAGTGGGCAACCAGCACTCTAGGCGCTGCTCTGTCTATGGAGTAGCCATTCTTTTGTTCCTTTACTTTCTTAATAAACTTGCTTTCACTTAAAAAAA

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FIGURE 118

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1.stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLP LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSF SYPRQDWTGSTPAYGYWFKAVTETTKGAPVAT
NHQSREVE MSTRGRFQLTGDPAGKNC SLVIRDAQM QDESQYFFRVERGSYVTYNFMNDGFFLKVTVLSETPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINNVPT
AGPLAQKR NQKATPNSPRTPPPPGAPSPESKKNQKKYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ

Important features:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

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FIGURE 119

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCTTGGGGGGCCTCCGGGATTGCTACCTTTT
TGGCTCCCTGCTCGTGAACCTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGAGCAGGCGAATCGCACTGGAGGCCCTCTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCAGTGTTCCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAATCTGGAGACGCGGGATATGATTGGTTCGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA
CAAGGGTGTGTGGTCATCCTGCGCAAGGACAGCGCCAGTCGCTGGTGGTGGGAGGCCAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAAGAGCTGGGGGGTGTGTGTATGTGTACTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCAGATATTGCACTGGGTGCCCTTTGATGGTGGTGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGGTTGTGCGCAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGGAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCTCCTCCATGCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCACTCCC
CAGCAGCTATAGCCCTACTGTGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAAGCAACAGCACCAGGCCCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGGCCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGCAGGCTCCTGGCCAGGGGGTGCCTCCAGTGGC
CCCCATCCTCAATGCCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCCCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACCGGCTTCTGTACCCGGGTGAGGACACCGGAATTCCAACC
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCCTGAGTGGGAGCCAGTCAATTGGCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGGCTGATGGGGATGATGCCATGAAGCCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT
CTTTAGCACCTCCGGGATCAGCATTGAGACCAGGAGTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTCTGGTGTGGTGGGGGCGAGAGACCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCCGCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTGTGTACCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGGCGGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGAGCGGAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGTC
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGCTGCCACTCTA
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGT
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCGGCGGGAGGGCCCCGATGCACA
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCGATGGGCATCCAGGGCCAGGCACCGCCTAGGTTCC
CATGTCCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGCATCAAGATTTGGCAGGATCGGCTTCTCCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCTCCCACCCAACTTCCCCTTAGAGTGCTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
TGAGAAGGGCAGGGGTGTCTGATGCAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCTTAACCTAGAGGGTGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTTATTAATAAATATTTGAGAACAAAAAAAAAAAAAAAAAAAA

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FIGURE 120

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQLQPRPQSWLLVGAP
QALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWLGVSVRSQGPQGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCGRPOGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGT
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRILPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVI
LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGDLNQDGFDPDIAGAPFDGDGKVFIYHGSSSLGVVAKPSQVLEGEAVGIKSFYGSLSGS
LDMMDGNQYPDLLVGSLADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGGHSVCVDLRVCF SYIAVPSSYSPT
VALDYVLDADTDRRLRGQVPRVTFLSRNLEEPKHQASGT VWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPQGGLPPVAPILNAHQ PSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALSGQP VIGLELMVTNLPSDPAQPPQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSNENASHV
ECELGNPMKRGAQVTFYILISTSGIS IETTELEV ELLLATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVRGERAMQSERDVGSKVKYEVT VSNQGQSLRTLGS AFLNIMWPHEIANGKWLLYPMQVELEGGQGPQKGLCS
PRPNILHLDVDSRDRRRRRELEPPEQQEPGERQEPSMSWWPVS SAEKKKNITLDCARGTANCVVFSCLY SFDRAA
VLHVWGRLWNSTFLEEYS AVKSLEVIVRANITVKSSIKNLMLRDASTVIPVMVYLDPM AVVAEGVPWWVILLAVL
AGLLVLALLVLLWKMGGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTG TILRNNWGSPRREGPD AHPILAAD
GHPELGPDGHPGPGTA
```

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 121

GGCACGAGGCGGCGGGGCGAGTCGCGGGGATGCGCCCCGGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCAGCAGCTTTAGCCCATGAGGAGGATGT
GACCGGGGACTGAGTCAGGAGCCCTCTGGAAGCATGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA
TCTTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC
GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAACTGG
ACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC
TCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGACAGAGAAGCTTGTGGCCATGACAATGGGCT
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGACGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG
ATGATGTTGTGAAGTCGATGTACCCTCCGTTGGACCCCAAACCTCCTGGACGCACGGACGACTGCCCTGCTCCTGT
CTGTGAGTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACCAGTCTC
TGTCGGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCTCCCAG
GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTGAGTTTATGCCTCTTTTGAGTTGCAAACCTGTGGCTGGT
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC
TGTCAGCTTTATTTAGCTCACCTAGTGTTCAGAAAATGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT
TAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATGTGTGGCAATTCTGATCTGCATTTTCAGAAGAGGAC
AATCAATTGAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATT
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGGTTTGGGTTTGAAGCTGAGGAAC
TACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT
ATACTTATGTTCCCTCAAAAAAAAAAAAAAA

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FIGURE 122

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHIE
AILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
DPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 123

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCCGCCGGGGGCGCAGCGCCCGAGCCGCGGCC
CTCGAGACGGGACCGAGAGCATCATGGGCCAGCACTGTCCCGCGCTCCGCCTCCGTGCTGCTTCTGCTGCTGCTCC
TGCGCCGGGCGGAGCAGCCCTGCGGGGCGGAGCTCACCTTCGAGCTGCCGGACAACGCCAAGCAGTGCTTCCACG
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT
ATGTAGAGGACCCCGAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG
AAGTCAAGGGCGTTTATCAGTTTTGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTCACCCAGATGGAGTCCG
CCTGCGTGACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCAGACGCATTACCGGCTGCGGGAGGCCCAGG
ACCGGGCCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTCTGCG
TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTCACAGAAAAACGACCCATCAGCAGGGCAGTCCACTCCT
AGCCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTCACAGCCTGCTGGGCT
GGTTCGCGTAGCCAGGGTGGAGGCAGAACGATGCTGTGGTAGCCCTTTGCCTTTTCATGCCCATGCTTGATT
CTTGACCTCAGCAGCTGAAGGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGCAGCGCTG
AAAAGACATTTACAAC TAGGCCAGGGATTAGCCACTGTGGGAGGGTGGACAGGCAATGGTTCAGTGGCCTGGCTG
TTGGCAGGAAC TCCAAGTGGCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCCTCTGTTTCATGATGCATGGGTCT
TTGTCTTGGGTGTCCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT
GTACCTGAGGAAACCAGGCCCTGGGTGACTTTGCAGATCTGCTCACCTCGGTGAGCAACAGTGTACCCATGCA
AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAAC TGTGGGAAACTG
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 124

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052

<subunit 1 of 1, 217 aa, 1 stop

<MW: 24777, pI: 5.55, NX(S/T): 0

MGSTVPRSASVLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG

GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSSHKTIVYFDFQV

GDEPPILPDMGNRVLTALTQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS

YWSVGETIALFVVSFSQVLLLSFFTEKRPISRVAHS

Important features:**Signal peptide:**

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32, 48-54, 131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

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FIGURE 125

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTGAGCCCATTTGGCCCCGACGCCTCTGT
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG
GAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGTCAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT
CAGGCTTCCTGCTTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTCCCCTTCTACT
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAACGCCCGCTGGCTGGAAC
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGGAGGTACCAGGCA
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT
TCCGCTACCATGGGCTGTCTCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG
CCCTGGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAA
AAAAAA

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FIGURE 126

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKVMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISMGC AFINLCILASQ
HAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRITTAAMWALQTVEKERGLGGEVPGSHQGPDPYRQLREKDPKY
SALRQNFERYHGLSSICNLGCVLSNGLCLAGLALEIRSL**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

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FIGURE 127

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGC
CATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTCCTGTTCTTTGG
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAAT
TGGTTTAGAAAGAACATTTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAGGGG
CTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG
ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACAAGTGAATTTGAAGACTCATTTAAAATA
TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAATGTTCTT
TACAGGAGTTTAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTA
CTCAAGTGAAGTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTGAAATCCATGTTAATGATGCTTAAGAACTC
TTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT
TTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTTGAAGTGTCCACTGCAATGGCAAAAA
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAC
CAAGGAAACCCAATTTTGATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

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FIGURE 128

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHMKATGFFLGGV
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGIRSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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FIGURE 129

AATTCAGATTTTAAAGCCCATCTGCAGTGGAAATTCATGAACTAGCAAGAGGACACCATCTTCTGTATTATACA
AGAAAGGAGTGTACCTATCACACACAGGGGAAAAATGCTCTTTTGGGTGCTAGGCCTCCTAATCCTCTGTGGTT
TTCTGTGGACTCGTAAAGGAAAACCTAAAGATTGAAGACATCACTGATAAGTACATTTTTATCACTGGATGTGACT
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTCATGTAATCGCTGCCTGTCTGACTGAAT
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA
ATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG
GTGTTCCCGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT
TTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA
GTGTTGGAGGTGCGCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAGGTTTCAATGACA
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACCTCTCATGCATTGAACCAGGATTGTTCAAAACAACTTGG
CAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAAACAACATATG
GAGAAGGTTACATTGAAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG
TGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGG
CTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTAGATCGTGCTTATTTGGATTGCAAA
AGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGT
ACATCACATAGGCAAGTCTGCCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT
GCCCATTCAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGT
TAAGTATCATCTTATCTAATATTAAAGATAAGTCAACCCAAAAA
AA
AAAAAAA

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FIGURE 130

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGLLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENVKRTAQWVKNOVGEKGLWGLINNAGVPGVLAPTDLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMKAFGVHVSCIEPGLFKNLADPVKVIEKKLA
IWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLKQKAELANPKAV

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 131

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA
TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTTGGTGAAGTTTTTCATTCCCTC
AGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT
ATGAATTTGCAAAACGACAGAGCATATTGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG
AGTGCCGAAAAC TAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC
TAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC
TTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTGGATCACAAAAG
CACTTCTTCCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA
TTCCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTC
AGGCCTTGGGAAAAC TAGGTATCAAACTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCAACAAAATC
CAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA
AGAAAATGATTTTTGTCCATCGTATATCAATATCTTCTGAGACTACAGAAGTTTCTTCTGAACGCGCCTCAG
CGATTTTAAATCGTATGCAGAAATATTC AATTTGAAGCAGTGGTTGGCCACAAAATCAAATGAAATGAATAAATA
AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCAATCAATGCTGCAAAGCTTTATTTACAT
TTTTTCAGTCCTGATAATATTTAAAACATTGGTTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT
CTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTTTTCATGCCTCTTAAAACTTCTG
TGCTTACATAAACATACTTAAAAGTTTTCTTTAAGATATTTTATTTTCCATTTAAAGGTGGACAAAAGCTACC
TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTG
TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT
TATCTCAACCTGGACATATTTTAAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCTTTTCATTAGCCCAA
AACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTATAACTCTGAAGTCCACCAAAGTGGA
CCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA
GAATTTTAAAGTTCTAGCCCCATGATAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGAT
GTTTAGACAATTTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAACA
ATGGACCCAAGAGAAGAA

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FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSSILVLWDINKRGVEE
TAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNILGHFW
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLI PYCSSKFAAVGFHRGLTSELQALGKTGIKTSCLCPV FVNTGF
TKNPSTRLWFPVLETDEVVRSLIDGILTNNKMFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:**Signal peptide:**

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FIGURE 133

CTGAGGCGGCGGTAGCAATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT
CCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAAGGTGAAGCCAAGAACAGCAT
TACTGATTCCTCAATGGATGATGTTGAAGTTGTTTATACAATTGACATTGAGAAATATATTCCATGCTATCAGCT
TTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA
TGTGGTAGGTTGGTACAAATCCGTCGTCATTGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAA
CTTGCAGGAGCATTTCACCAAGACCTTGTTTTCTGCTATTAAACCAAGTATAATAACAGAAAAGCTGCTC
TACTCATCGACTGGAACATTCCTTATATAAACCTCAAAAAGGACTTTTTACAGGGTACCTTTAGTGGTTGCCAA
TCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGT
ACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC
TTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA
GGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGGCAGCAAGAGAGAAGAACAT
CCAAAAGACCCCTCAGGAGAACATTTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCA
TTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAGCTAGTCCAGCTAGTACACCACAAATCATTA
GCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATC
TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCCAGAAAACAGATGAAGAAATTGA
AAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACATTTGATCCTTTTAACTTACAAGGAGATTTTTTT
ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCATTTGTT
TTTACTATGTTACCTGTTTGAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAA
CATCAGATGCTTTTATTTCCAAACCTTTTTTTCACCTTTCACCTAAGTTGTTGAGGGGAAGGCTTACACAGACACA
TTCTTTAGAAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCAGCACTTAGGGAAGACAAGTC
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAA
ATGGAAGCAAGAATAGCCTTATTTCAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAAAA
TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAATGCTGGATATCATGCAAT
AAATTTGCAAAACATCATCTAAATTTAAAAA

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FIGURE 134

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYITIDIQKIIPCYQLFSFYN
SSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERILLHKNLQEHFSNQDLVFLLLTPSIITESCSTHRLE
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEDGSLKEVHKINEMYASLQEE
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS
LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQDKRSKANTG
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

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FIGURE 135

GGCACAGCCGCGCGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC
CAAGCAGCGCGCAGCGAACGCCCCGCGCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCTCC
TTCCCCGCGTCCCCGCTCGCCGGCCAGTCAGCTTGCCGGGTTCGCTGCCCGCGAAACCCGAGGTACCCAGCC
CGCGCCTCTGCTTCCCTGGGCCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGGCGCCTGGCACCGGGG
ACCGTTGCCTGACGCGAGGCCAGCTCTACTTTTCCGCCCGCGTCTCCTCCGCTGCTCGCCTCTTCCACCAACT
CCAACCTCCTTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGCG
TTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGCGCCGCGCACCATGGCACGGTTTCGGCTTGCCCGCGCTT
CTCTGCACCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA
CGTCTTTACGTGTCCAAAGGCTTCAACAAGAAGCATGCCCCCTCCACGAGATCAACGGTGATCATTTGAAGATC
TGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA
AGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTTCTT
AAAGAAGTACTTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAA
AATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA
ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCTGGTGAACCTCCAGTACCCTTTACAGAT
GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCTCGCAATTTGAAGCTC
CAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTGCTCAAGGCTTAGCGGTTGCGGGAGATGTCGTGAGCAAG
GTCTCCGTGGTAAACCCACAGCCAGTGTACCCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGGT
CTCGTGAAGTGTGAAGCCATGTTACAATACTGCTCAACATCATGAGAGGCTGTTTGCCCAACCAAGGGGATCTC
GATTTTGAATGGAACAATTTATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCTTTCAACATTGAA
TCGGTTCATGGATCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT
CAGAAGGTTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGTTCCATCTCTGAAAGT
GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA
CTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATTTCTGGTCTCCCTTCCGAGCAACGTTTGAAC
GATGAGAGGATGGCTGCAGGAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT
GCAGTGACAGGAAATGGATTAGCCAACCAGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAACACAGACATA
CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAGTGGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA
GAGTTTGAATACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCCT
GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCCTGGTTATGCAGAGAGAGTGGAGATTAATTTCTCA
AACTCTGAGAAAAAGTGTTCATCAAAAAGTTAAAGGACCAAGTTATCACTTTTCTACCATCTAGTGACTTTGC
TTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGTGACTTTGTTTTT
TCATTCAGTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGTTTCTGCTCCCCCAAACCATGTTAAACGTGGCT
AACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTGTATGTTTTT
TTCTCATTTTCGTTTGTGGGTTTTTTTTTCCAAGTGTGATCTCGCCTTGTTCCTTACAAGCAAACAGGGTCCCTT
CTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTTATTATCATGTTATC
TTATTTAAAGAAAAAGCCCAAAAGC

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FIGURE 136

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPIHEINGDHLKICPQGSTCCSQEMEKEY
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSELFKDLFVELKRY
VVGNNVLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGL
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAE
RLEGPFNIESVMDPIDVKISDAIMNMQDNSVQVSQKVFQCGPPKPLPAGRISRSISESAFSARFRPHHPEERPT
TAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEV
QVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 137

GCGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCTCTCAGTCGGA
CTTCCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCCTGTAGTCATGTACCCACCGCCGCCGCC
GCCGCTCATCGGGAATTACCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCG
GCGCTCGTGTGGAGGAAATGGAAGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTCTCTCTGCTTTCT
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGAAGA
GCAGAAGATGAGGCCAGAAATTGCTGGGTAAAAACCAGCAATCCACCCGTCTTACCAGCTCCTCAGAAGGCGGA
CACCGACCCTGAGAACTTACCTGAGATTTGTCACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT
GCAGATTAGACCCCAAGCCAAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCTGT
GGATCCCCGCCCGGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGG
CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGGCACACC
AGTGCACTGAAGTATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGAAAGGATACCGCAAGTTTGC
ATGGGGCCATGACGAGCTGAAGCCTGTGTCAGTCTTCCAGTGGTGGTGGCTCGGTCTCACATGATCGA
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTT
ACACTTTGAAAAGGACGTGGACGTCAACCTGTTTGAAGCAGCATCCGCATCTTGGGGGGCTCCTGAGTGCCTA
CCACCTGTCTGGGGACAGCCTCTTCTGAGGAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAAGAC
ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCCACCGGCCACGGTGGACCTCCGACAG
CACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGGGAGCTCTCCGTCTCACAGGGGATAAGAAGTTTCA
GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCA
CAATACCCACAGTGGCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA
CCTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG
TGTCAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTGTGGGGGAGCTTGCCACGGCCGCTT
CAGTGCCAAAGATGGACCACCTGGTGTGCTTCTGCCAGGGACGCTGGCTCTGGGCGTCTACACAGGCTGCCCGC
CAGCCACATGGAGCTGGCCAGGAGCTCATGGAGACTTGTACAGATGAACCGGCAGATGGAGACGGGGCTGAG
TCCCAGATCGTGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA
CAACCTGTGCGGCCAGAGACCTGGAGAGCCTGTCTACCTGTACCGCTCACAGGGGACCGCAATACAGGA
CTGGGGCTGGGAGATTCTGCAGAGCTTACGCCGATTACACGGGTCCCCTCGGGTGGCTATTCTTCCATCAACAA
TGTCCAGGATCCTCAGAAGCCCGAGCCTAGGGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCT
GTTCTTGCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCTACGTGTTCAACACCGAAGCCACCCCTCT
GCCTATCTGGACCCCTGCCTAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGAGAGGACCTTGCTGGG
TCTGTGGCATTTTCCAAGGGGCCACGTAGCACCGGCAACCGCAAGTGGCCAGGCTCTGAAGTGGCTCTGGGCT
CCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAGGCCGTGAGTCTTGGTGTGATGCGGGGTGGG
CTGGGCGCTGGAGCCTCCGCTGCTTCTCCAGAAGACACGAATCATGACTCAGATTGCTGAAGCCTGAGCAG
GTCTCTGTGGGCCGACAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGT
GCAGCTCTGCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG
GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTCCTGGCCGCCCGCAGGGGGCT
TGGAGGGCTGGACGGCAAGTCCGTCTAGCTCAGGGGCCCTCCAGTGGAAATGGGTCTTTTCGGTGGAGATAAAG
TTGATTTGCTCTAACCGCAA

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FIGURE 138

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLSEEQKMRPEIAGLKPANPPVLPAPQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTOEEATKRQEAAPVDPPEGDPQRTVISWRGAVIEPEQGTELPSRR
AEVPTKPPPLPPARTQGTTPVHLNRYRQKGVLDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWI
LGLRKEFEEARKWVSKKLHFEKDVDVNLFESTITIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAHPPRWTS DSTVAEVT SIQLEFREL SRLTGDKKFQEAVEKVTQH IHG LSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLKQW IQGGKQETQLLEDYVEAIEGV RTHLLRHSEPSKLT FVGELAHGRFSAKMDHL
VCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPEIVHFNLYPQGRRDVEVKPADRHNLRLPET
VESLFYLYRV TGD RKYQDWGWEILQSFSRFRTRVP SGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDD
PNLLSLDAYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

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FIGURE 139

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG
CGATGAAAGTTCTAATCTCTTCCCTCCTCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA
ATCCAGGGGTGCGCCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT
GTGAGTGCAAAGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAAGAAGCAGT
GCCCCGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATT
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC
CCTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTC
ACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGT
TGCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC
CTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAC
AGAAGTCAATAAATATTTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 140

MKVLISL L L L L L P L M L M S M V S S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K F M T V S G L P K K Q C
P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

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FIGURE 141

AATGGCTGCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAACAGAACTCATTTTGAACACCCTGACTGCATTTTGC
TTTGTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 142

MAVLVLRITVVLGLLVLFITCYADDKPKPKDDKPDGKPKPDFPKFLSLLGTEIIENAVEFILRSMSRSTGFM
EFDDNEGKHSSK

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FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CCATGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTCTTCTTACCCTGCCCCTGACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTGTGCTCTG
TGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCACCTGAAAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTCCCAAGCT
CCAAGGCATCTATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCTTAGCAGAATGAGAGAAGACATTATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCCTT
CGTTCCTATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCTCTCCCCACTACCACCTTCTTCCCTGAGCTGGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTT
TAATAAATAGACGAAACCACG

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FIGURE 144

MDILVPLLQLLVLLLTPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQLKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCVS
QSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLPVGPHINGKAVKQSFSSKALICSFPSLQLEQATHQPIYLPRLGT

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FIGURE 145

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
TTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA
AGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
ACTTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATGTAGGGCCTCAACCTATAGACT
TTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTGAAG
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTG
TTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
TTGTCAATTTTGACCCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTT
TAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAAGAGATT
GTGATTCAGCCTCTACTAAAGTTGTCTATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA
AAAAGGAAAGAATTCTGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAAC
TGACGGAATGGAACGACAGAATATAACTAACCAGTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGT
ATAGCAGAACCCTGGCTGGTAGCATCACACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
ATCCTATGTGGAATGTCCGCCACCTTGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCA
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT
ATATTCCAGACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTCAAAACAGAA
TTTGAAGTGTAAAGCAAGCATTTCTCAGGAAGTCCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC
AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGCTAGGTAAGATGACAAACTGCCCTGTCTGGCAGT
CAGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTTTCTTACTACAATGCTG
AATGACTGGAAAGAAGAACTGATATGGCTAGTTGAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTA
ATTTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTC

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FIGURE 146

MSFRKVNIILVLAVALFLLVLHNFSLSSLLRNEVTD SGIVGPQPIDFVPNALRHAVDGRQEEIPV VIAASED
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKV KEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKV VIRGAGNQYNYIGYLDYK
KERIRKLSMKASTCSFNPGVFVANLTEWKRONITNQLEKWMKLNVEEGLYSRTL AGSITTPPLLIVFYQQHSTID
PMWNVRHLGSSAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 147

GTTCGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA
AGTCATTTCCCTTATTTAACCAGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA
ATGATGTTGACACCTCCACCGAATTCTAAGTGGAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCAACACCCTTCTGGTTCACATTTTCATTT
CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
GCATAGAATTGGACACAGAAAGGGAAAAATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG
CAGTGCTGCTCGTCTTGATTTTGTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
AAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC
TCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGGAATATA
AGCCCCTTTCGGGCATTTCGGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATC
ATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTAAATCT
CTGTGGTGAGGATTCCGAGAATCATTGTGATGACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
CATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCTTGTTCCAAGA
ACTCAAGTCACCTTTACATCTATTAAGTGTCTTGGAGACTTCATAATTTTCTAGGAAAGGTGTTAGTGGTGTGTT
TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG
TAGCTTTTTTGCCTACTTAGTAGCCCATAGTTTTTATCTGTGTTTGAACTGTGCTGGATGCACCTTTCCTGT
GTTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
TCGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGAGGGAA
CAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
TTTACAGAATAGAAGATGAGACCCTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCT
TTCCTCAAAA

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FIGURE 148

MSGRDTILGLCILALALSLAMMFTFRFITLLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIELDTERENMKC
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY
HQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPLLLVAFFAYLVAHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

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FIGURE 149

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGGTTCTTGACCTCTCCCTGTTTCTTCTTAGAATAATTTGTA
TGGGATTTGTGATGCAGGAAAGCCTAAGGGAAAAAGAATATTCTGTGTGGTGAAAATTTTTTGAAAAAAA
ATTGCCTTCTTCAAACAAGGGTGTCATTCTGATATTTATGAGGACTGTGTTCTCACTATGAAGGCATCTGTTAT
TGAAATGTTTCCTTGTTTTGCTGGTGACTGGAGTACATTCAAAACAAAGAAACGGCAAAGAAGATTAAAAGGCCAA
GTTCACTGTGCCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCTGAGTTCATTGTGAAATGTCC
AGCAGGATGCCAAGACCCCAAATACCATGTTTATGGCACTGACGTGTATGCATCCTACTCCAGTGTGTGTGGCGC
TGCCGTACACAGTGGTGTGCTTGATAATTCAGGAGGGGAAAATACTTGTTCGGAAGGTTGCTGGACAGTCTGGTTA
CAAAGGGAGTTATCCAACGGTGTCCAATCGTTATCCCTACCACGATGGAGAGAATCCTTTATCGTCTTAGAAAG
TAAACCCAAAAAGGGTGTAACCTACCATCAGCTCTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGG
TGAGACCACAAAAGCCTATCAGAGGCCACCTATTCCAGGGACAACATGCACAGCCGGTCACTCTGATGCAGCTTCT
GGCTGTCACTGTAGCTGTGGCCACCCCAACCACTTGCCAAAGGCCATCCCTTCTGCTGCTTCTACCACAGCAT
CCCCAGACCACAAATCAGTGGGCCACAGGAGCCAGGAGATGGATCTCTGGTCCACTGCCACCTACACAAGCAGCCA
AAACAGGCCCAGAGCTGATCCAGGTATCCAAGGCAAGATCCTTCAGGAGCTGCCTTCCAGAAACCTGTTGGAGC
GGATGTGAGCCTGGGACTTGTTCCAAAAGAAGAATTGAGCACACAGTCTTGGAGCCAGTATCCCTGGGAGATCC
AAACTGCAAAATTGACTTGTCTGTTTTAATTGATGGGAGCACCAGCATTTGGCAAACGGCGATTCCGAATCCAGAA
GCAGCTCCTGGCTGATGTTGCCAAAGCTCTTGACATTGGCCCTGCCGCTCCACTGATGGGTGTTGTCCAGTATGG
AGACAACCTGCTACTCACTTTAACTCAAGACACACAGAACTTCGAGATCTGAAGACAGCCATAGAGAAAAT
TACTCAGAGAGGAGGACTTTCTAATGTAGGTGGGCCATCTCCTTTGTGACCAAGAAGTCTTTTTCCAAAGCCAA
TGGAAACAGAAGCGGGGCTCCCAATGTGGTGGTGGTATGGTGGATGGCTGGCCACGGACAAAGTGGAGGAGGC
TTCAAGACTTGCAGAGAGTCAGGAATCAACATTTCTTCATCACCATTGAAGGTGCTGCTGAAAATGAGAAGCA
GTATGTGGTGGAGCCCACTTTGCAAAACAAGGCCGTGTGAGAACAACGGCTTCTACTCGCTCCACGTGCAGAG
CTGGTTTGGCTCCACAAGACCTGACGCTCTGGTGAAGCGGGTCTGCGACACTGACCGCTGGCCTGCAGCAA
GACCTGCTTGAACCTGGCTGACATTGGCTTCGTCATCGACGGCTCCAGCAGTGTGGGGACGGGCAACTTCCGCAC
CGTCTCCAGTTTGTGACCAACCTCACCAAAGAGTTTGTAGATTTCCGACACGGACACGGCATCGGGGCCGTGCA
GTACACCTACGAACAGCGGCTGGAGTTTGGGTTGACAAAGTACAGCAGCAAGCCTGACATCTCAACGCCATCAA
GAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGGGGGCTGCCATCAACTTCGCCCTGGAGCAGCTCTTCAAGAA
GTCCAAGCCCAACAAGAGGAAGTTAATGATCCTCATCCGACGGGAGGTCTACGACGACGTCGGGATCCCAGC
CATGGCTGCCCATCTGAAGGGAGTGATCACCTATGCGATAGGCGTTGCCCTGGGCTGCCAAGAGGAGCTAGAAGT
CATTGCCACTCACCCCGCCAGAGACCACTCCTTCTTTGTGGACGAGTTTGACAACCTCCATCAGTATGTCCCCAG
GATCATCCAGAACATTTGTACAGAGTTCAACTCACAGCCTCGGAAC**TGA**ATTAGAGCAGGCAGAGCACCAGCAA
GTGCTGCTTTACTAACTGACGTGTTGGACCACCCACCGCTTAATGGGGCAGGCACGGTGCATCAAGTCTTGGGC
AGGGCATGGAGAAACAAATGTCTGTATTATTCTTGGCATCATGCTTTTTCATATTCCAAAACCTGGAGTTAC
AAAGATGATCACAAACGTATAGAATGAGCCAAAAGGTACATCATGTTGAGGGTGTGGAGATTTTACATTTTGA
CAATTGTTTTCAAATAAATGTTTCGGAATACAGTGCAGCCCTTACGACAGGCTTACGTAGAGCTTTTGTGAGATT
TTTAAGTTGTTATTTCTGATTTGAACTCTGTAACCTCAGCAAGTTTCATTTTTGTGATGACAATGTAGGAATTG
CTGAATTAATGTTTAGAAGGATGAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSLSLPRWRESFIVLESKPKKGVTYPSAL
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQ
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTHTNSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNEFFSKANGNRSGAPNVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKEF
EISDTDTRIGAVQYTYEQRLEFGFDKYSSKPDILNAIKRVGYWSGGTSTGAAINFALEQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSFFVDEFDNLHQYVPRITQNICTEFNSQPRN

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FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCCTTTCCGGCT
GCTCATCCCGCTCGGCCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGTGCGCCAGGTCCCGACGGCTCCGCGCC
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGAATGTCTC
AGAATTCCAAAGAGTGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGA
AACAAACATTGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAGTAGAGGC
TGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCGGAAAACCTCCTCCAGCCTTTAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTCACCTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGT
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTGGCAACCACATGATGTGCT
CACTGGCAAGTGGGTGGCCCAGGACGCGAGGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAGCCATCCGGAACCTACACCCG
CTTCGATGACTGGTACCTGTGGGTTGAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCTTGGAGGC
CTACTGGCCTGGTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGT
ATGGAAGCAGTTTGGGGGGCTCCCGGAATTCTACAACATTCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA
CCCACTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCCTCCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGGGATTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG
GGCTGGGGGGGTACATCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCGCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGCAAAATTCAGAA
AAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCACTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTCATAACCACTGGATAATTTTTTTATTTTTATTTTTTGGAGCT
AACTATAATAAATTGCTTTTGGCTATCATAAAA

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FIGURE 152

MPFRLLIPLGLLCALLPQHAGAPGPDGSAPDPAHYSFSLTLIDALDITLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPILLMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMVPVQSLEAYWPGLQSLIGDIDNAMRTFL
NYYTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECGFAT
IKDLRDHKLDRNMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPPTLFS PENHDQAREKPAKQKVPLLSCPSQP
FTSKLALLGQVFLDSS

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FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCTTCGT
CACTCACCTGTTCTTGCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG
CCTATTTCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGTGTAGAGACAGATGGTGATGGGGGATTCATGGTGAGCTAAGGAGAGGGTGGTGGCAG
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGTCAAGGAGT
TAAAAACCCTAGAAAGCAAAAGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTT
TGAGGGTGCCCTCCCAAGCCTGGGAGTAACATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTTCAGAGAGGAGATCTGGGTGGGAAAAAGATG
GGGCAAGCGGTATGATGCCTGGCAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT
CCATGTTTCCTAACAGATTCAAGTCTGGCCAGGTGTGGTGGCCACACCTGTAATTTAGCACTTTGGGAGGC
CAAGGTGGGAGATCACTTGAGGTGAGGAGTTCAGACAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA
AAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCACAGTAACATCATGCCTGTAATCCCAACATTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCATCTCTAAATAAATGTTTTAAAAAT

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FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSFNLDEHHPRLLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPPSGDRRGDVYR
CPVGGAHNAPCAKGHLDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS
```

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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FIGURE 155

GCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC
AGCGTCCCCGCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAAACAAGCCTGGCAGG
GTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAATAATGCTGCTTTGGTTGAT
ATTTTTCACCCCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCAGTTGAGAAAGGT
ACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGATTTGAGGCAGATGCTAAGATGATGGTAAA
TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGCCTTTCTGAATTGGAGGATTATCTTTCCTA
TGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA
AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTGAGCATCTT
GGACAAAAGGTTCTTAACCAATTTCCCTTTGAGCAGAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTCTCAT
TTCCCTCAGCATGTTCTAACTGCTGCCCAGTGTGTTGATGGAAGGACTATGTCAAAGGGAGTAAAAAGCT
AAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA
AAAATCTGGCCGGGGTCCAGAGGATTGCCGAAGGGAGGCCTTCCCTTCAGTGGACCCGGGTCAAGAATACCCACAT
TCCGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGAGCTGAAGCG
TGCTCACAAAAGAAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGAATGATCCACTT
CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGTCAGTGTGTCCGACGAATCCAATGATCT
CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
AAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTGAGAAGGA
CTACAACGTTGCTGTTGCGATCACTCCCTAAAATACGCCCAGATTTGCCTCTGGATTACGGGAACGATGCCAA
TTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACAGCTCTGCTTA
CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACCTCTGTCAATAGCATTTCACATTTTCAAATCA
GGAGATTTTCGTCCATTTAAAAATGTATAGGTGCAGATATTGAACTAGGTGGGCACTTCAATGCCAAGTATAT
ACTCTTCTTTACATGGTGATGAGTTTCATTTGTAGAAAATTTTGTGCTTCTTAAAAATTAGACACACTTTAA
ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTACTCTAAGAAGAAT
CTAATAGGATGCTGTTGTGTATTAAATGTGAAATTGCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
ATAGAGACAGAAAAGTTACAACACAGTTTGTACTACTCTGAGATGGATCCATTGAGTCTATGCCCTCAATGTTTAT
ATTGTGTTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTTGAAGAATTACAAATCAGAAGAAAAGCAAGC
ATTATAAACAAACTAATAACTGTTTTACTGCTTTAAGAAAATAACAATTACAATGTGTATTATTAAAAATGGGA
GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
TTTAACTAATACTCAAAATATGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTATAGGACAAAGAATTCTGTAA
TCTTTTTCAAGAAAGAGTCTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCCTG
ATTAGTAATTTTAGATATGTCCTTCTCTAAAATGAATAAAATTTATGAATATGA

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FIGURE 156

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRFLTNFPFSTAVKL
STGCSGILISPQHVLTAACHVHDGKDYVKGSKKLRVGLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGRRRRKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCVSDSNLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKRKIIAVYSGHQW
VDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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FIGURE 157

GGGACCCATGCGGGCCGTGACCCCCGGCTCCCTAGAGGGCCAGCGCAGCCGAGCGGGACAAAGGAGCATGTCCGCG
CCGGGGAAGGCCCGCTCCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGGGCCCCGCGCCGCGCTCCTGCCCGCCCC
GGCTCCGGGGCGGGCCCGCTAGGCCAGTGCGCCGCCGCTCGCCCCGAGGCCCGGCCGCGAGCATGGAGCCACCC
GGACGCCGGCGGGGCCGCGCAGCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
GGCGCGGGCGGGCGGGCGCGCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGCAGG
GCGGCGGGCGCGGCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCTGCCCCAGATACTCTG
CCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTA
AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA
TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCAGGACTCACCAAT
CTGTTTCGGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTTGATTATCTTGGCTCATT
CGGTCCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGGTAAAGGAG
AAGAACATCACGGTACGGGATACAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACCACTCACAGGCGTGAA
CAGGAGCTGTTGACATGCGACCTCCGCTTGAAATGCGCTCTTCTACATGACTCCATCTCATGCCAAGTTGTG
TTTGAAGGAGACAGCCTTCCTTTCCAGTGCAATGGCTTCATATATTGATCAGGACATGCAAGTGTGTTGGTATCAG
GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAATGATTACAACTGCTCCTTG
ATTGCAAGTGCCCTAACCATTTCTAATATTACGGCTGGATCTACTGGAAATTTGGGGCTGTCTGTCAGACCAAA
CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCCTCCAGGAGGGTG
GTAAACAACAAGGTGACTTCAGATGGCCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAAC
ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC
TTTTGGGCAGATGATGATTATTCTCGCTGTGAGTATGCAATGATGTCACTAGAGTTCTTTATATGTTAATCAG
ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACCTT
TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
AAAGAGCTAGGTGACGTGATGGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG
CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGG
GCTCACGTTTATTCAACATATTACCCAAATATTGCTCTGGAAGCTTATGTCATCAAGTCTACTGGCTTCACGGGG
ATGACCTGTACCGTGTCCAGAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
TGTTACATTCTGCAATCATTTAAGACTATTTACAGTAAATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA
CCTTATTAAGATTTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGTCTACTGTTTTAAAGAAAATAACCA
GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCTTTGATTCCCTTTCTTCACATAAAAAATATCA
GAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACTATTGTTACATGTGAAAAATTTTATTTGACT
TAAAGTTTATTTATTTGTTTTTTGCTCCTGATTTTAAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATC
ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGAGAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGC
TGTATATCAAAATTTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTATTGAAGCA
AGCAAAATGAAAGCATTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTTGACTACACTGTATTGAAGCAA
ATAGAGGAGGCACAACCTCCAGCACCCCTAATGGAACCACATTTTTTCACTTAGCTTCTGTGGGCATGTGTAATT
GTATCTCTGCGGTTTTTAAATCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCC
AGTCATTTTAAATGGCTGCATAATAACTGATCCAACAGGTGTAGGTGTTCTGGTTAGTGTGAGCACTCAATAAA
TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

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FIGURE 158

MEPPGRRRGRAQPPLLLPLSLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTLLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSLKRLDLTNNRIGCLNADIFR
GLTNLVRLNLSGNLFSSLSQGTFDYLASLSLEFQTEYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPELPSFYMTPSHRQVVFEGDSLPFQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIH
NCSLIASALTISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTL AGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNLTNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRETKEEKSKELGDMVDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:
amino acids 1-33

Transmembrane domain:
amino acids 13-40 (type II)

N-glycosylation site.
amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596

N-myristoylation site.
amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

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FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTT
CTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGAAAGTATTTATTGACCAAATTAACAGG
TCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTCTAGAGAAGAGGATCTAACT
CCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATC
ACTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTG
GAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCCATAATGGATG
GAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTT
TGGGAAGGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG
GTAAGGTCAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCA
GAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTGATGCAGAATACACCAAAAACAGGCC
TGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAAATACAAG
TATCTGTTTAAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCTGTGTGGCTCACTTGTTTTT
CATGTTGGTGATGAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGTCACTATATCCCAGTCAAAACA
GATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG
GGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTACTGGGAGAACCTCTTGAGTGAATAC
TCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTATTTCCCAAAATGTTGAAAACCTGAA
CTATAGTAGTCATCATAGGACCATAGTCCTCTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACC
ATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAG
AGCAACTCTTGAGAAAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGG
ACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCATTTCTTAAGACCAATCACAGCTTGTGCC
TCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTTGTCCCATTA
TTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTCATTTGCTGGAATTGTGAAATTATTCAAGGCGTGATC
TCTGTCACTTTATTTTAATGTAGGAAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTC
TAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTTTTGTAAAACCATAAACTCTGTACTCAGGA
GGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATTTTCAGGTTCCCTTTTT
GTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

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FIGURE 160

MEWWASSPLRLWLLLFLPSAQGRQKESGSKWKVFIDQINRSLNIEPCSSQNCSCYHGVIEEDLTPFRGGISRK
MMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPDMEMVINVRDYPQVPKWMEPAIPVFSF
SKTSEYHDIMYPAWTFWEGGPAVWPYPTGLGRWDLFREDLVRSAQWPWKKKNSTAYFRGSRTSPERDPLILLS
RKNPKLVDAEYTKNQAWKSMKDTLGKPAKDVHLVDHCKYKYLNFNFRGVAASFREKHLFLCGSLVFHVGDEWLEF
FYPQLKPWVHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSYNVT
RRKGYDQIIPKMLKTEL

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FIGURE 161

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
CCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA
CAACAAAAAATCTAAGCTTTAATTTCATCTGGAATTCCACAGTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCCGAGTGTAAGAACCTTCGGCTCG
CGTGCTTCTGAGCTGCTGTGGATGGCTCGGCTCTCTGGACTGTCCTCCGAGTAGGATGTCACTGAGATCCCTC
AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
ATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTACAGACAAGACTTCACTTCACACTTCGA
GAGATTCAAACCTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCC
AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTTCTTATTA
GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA
ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTCAAGTGGGTAAGTGA
TTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTCATCAATACTGGCAATTTAGTGAAGTAT
CTTTTAAACCTAAACCACTCAGAGAAGTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTT
TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTGGGTTAT
ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTT
TATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCATATTCAGAAAGACACAAATCTTTCTTTCTATAT
AGAATCCATTGGATGTCTGTCACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCAAGGAGATCATCACT
TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAAGTTTCACTTACATTCTACAAAAAGCCTAGAAGGACAGG
ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACT
GAACTGAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTTATTAGTCAGGCCCTTCAA
GATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAAAACAATTTG
GACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
AACAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
TTAAAAATATATGTAGTTCTGTGTCAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG
GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTTTAAATTAAGTTCACTTTGTGTT
TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATCTTTACATGCAACATTTTCCAGT
TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAAATGTAAAGTCATAGGTCATTATTGCATATCAGTA
ATCTCTTGGACTTTGTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAATCTGAAAA

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FIGURE 162

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLALSLEDEHLLYGDIIHQDFLD
TYNNLTTLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLNLNLHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLKVNHIHPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

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FIGURE 163

CATTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTACAGAAGTATATTAACTTTTTAGG
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
TCCTAGTATTAATTTCTTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG
AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTT
TGTTTACATGCAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTG
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCACTACCTTGCACTAGAGCACTTCAGATTCGGTTGCCAA
CTCGTCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
TTTATACCAGAAAAAGCCAAACTATGAATTACTGGAAGAAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
CCAAATTAAGCAAAGGGATTGAATCCGGATGGAATCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCT
CCAAGCCATCATCACCAAGAGAAGTAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAGTCAAAA
AAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGAC
ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAGCAAGC
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCT
TGGTTTTGCCTATCTACAGTGTGATGTATGGAATCAATCAAAAACATTAAACGCAAACTGATTAGGATTTGATTT
CTTGAAACCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTGAAAAGAACTATGTTAATTTTTTTGCACAT
TAAATGCCCTAGCAGTATCTAATTAAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
ATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTTATACAGATAAAATTGCAGACACTGT
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATT
TTTACAAGGAAATAAAATACAAATCTTGTTTTTTCTAAAAAAGT

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FIGURE 164

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSHSESPRRHHNHGSPHLKAKH
TRDDLKSSNRHGHKRRKSRSRSQSKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

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FIGURE 165

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCGTGATTTATTAACGTGGCTTA
ATCTGAAGGTTCTCAGTCAAATTTCTTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT
GGCTGGTTTGGGCCCTTGCTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGC
TTCTGTTGCTGGTCTTGCCCTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCTCTGTATT
CAGAACTCTGTAAAGGTGCCCTCCCACTACGGCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATTCTCTTAAATGACAG
ACGAGCCTGGCCTAGACAACCTGCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
CTGGCCGGAGCAACCGAAGTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
ATCGAGCTTTGAGTGTTCTTCGAAGGACAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCGACCAGGGCAGGGAAA
ATTCTGAAAACACCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACTGATTCCAGATGGTGAAATTACCAGCA
TCAAGATCAATCGAGTAGATCCCACTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC
ATATCATTTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGCGCCGGCTACTGCCAGGAGACATCATTC
TAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACACGCTGTGCGTCTCTGCGGCAGCCCTGCCAGG
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCCGAGCAGGAACAATGGACAGGCCCCGGATGCCACAGAC
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAAATAAACTGGTGCGCA
AGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
AGAATGACCGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAGTGCGGCTCATCTGATTC
AGGCCAGTGAAAGACGTGTTACCTCGTCTGTCCCGCCAGGTTCCGGCAGCGGAGCCCTGACATCTTTCAGGAAG
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGAGCAACACTCCCAAGCCCCCTCCATCCTA
CAATTACTTGTCTATGAGAAGGTGGTAAATATCCAAAAGACCCCGTGAATCTCTCGGCATGACCGTCGCAGGGG
GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCATCAGTGTGAGCCCGAGGAGTCATAAGCAGAGATG
GAAGAATAAAAACAGGTGACATTTTGTGAAATGTGGATGGGGTCCGAAGTACAGAGGTGAGCCGGAGTGAGGCAG
TGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAGCTTTGGAAGTCAAGAGTATGAGCCCCAGGAAG
ACTGCAGCAGCCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAACCTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA
TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGGCCTG
GCACTTTTTTATAGAAATCAATGATGGGTGAGAGGAAAACAGAAAATCACAAATAGGCTAAGAAGTTGAAACACT
ATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGATACATTGTAAAAATGTCAGGAAAAGTATGATCATCTAA
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTAAGTACTAGTTTTTTTTCAGTGTTGGAGGAT
TTCTCATTTACTCTACAACATTTTATATTTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATT
TGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
GGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTTCATCAACAAGAAT
AAATATTTTTTCAGAAGTTAAA

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FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPEVSAAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPEVFPRLYHLIPDGEITSIKINRVPSESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPG
DIILKVNMDISNVPHNYAVRLLRQPCQVLWLTMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVSRQVRQRSPDI
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVI
SRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFPIKSIVEGTPAYNDGRIRCGDILLAVNGRS
TSGMIHAACLARLLKELKGRITLTIVSWPGTFL

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FIGURE 167

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAGTTGATCCCAACCATAACATCGTGGAG
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCA
TGAATCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATTGGGAGGCCAACCCACAGAACAGCATT
CTGGGCCAGGCTGTAATCAGAATTGTCGTGCTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT
GTGGAGAAGTGATGATACTCTCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATT
CCTGTATCATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHLEWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGGOPTQHFWARL

FIGURE 169

[illegible]

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FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGTYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGIFYCAECRAGWYGGDCMRGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGFPVNGYQKITGGPGLI
NGRHAKIGTVVSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLY
SAAFSKQKLQSAPTCKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAIIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADLKVVLG
KFYRDDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
WNVLADVRSPGFKNDTLRSGVSVVDSSLCEEQHEDHGIPVSVTONMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLFPFKDWIERNMK

FIGURE 171

CTGTGCTCTTTGCTTCAGCCGCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
ATCCGTCTCCACCACAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
CACCACCATCACAAACCACCACGAGCTCATCTTCGGGCGCTGGGGTCCCCCATGATCGTGGGGTCCCCCTCGGCGCCCT
GACACAGCCCCTGGGTCTCCTTCGCCTGCTCGAGCTGGTGTCTACCTCGTGGCCCTCTCGCTGGTGGCTAGCGCT
GGGCGCCTGGACGGGGTCCATGGGCAACTGGTCAGTGTTCACCTGGTGCTTCTGCTTCTCCGTGACCCGTGATCAT
CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCCT
CTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCCTGTCCACGGCCG
TTCGCGGGGACCACGCCATCGCCGCCACCTTCTTCTCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCCTG
GACCCGGGGCCGGCCGGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGSTGCTGGAGACCTT
CGTTGCCTGCATCATCTTCGCGTTTCATCAGCGACCCCCAACCTGTACCAGCACAGCGGGCCCTGGAGTGGTGCCT
GGCGGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCT
ACCCATCCCCCTTCCCAGCTTCTCTGTGCGGGCTGGCCCTGCTGTCTGTCTCCTCTATGCCACCGCCCTTGTTC
CTGGCCCCCTCTACCAAGTTCGATGGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCGAG
CATGCCTACTACGTGTGTGCGCTGGGACCGCCAGTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTA
TGTGGCTGACCTGGTGCACCTCTGCCACCTGGTTTTTTGTCAAGGCTTAAGACTCTCCCAAGAGGCTCCCGTTCCC
TCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCTCCGCCCTTTCCTCTGTTTT
CTCTTCTGTCTCCCTCCCTCCCACCTTTTTCTTTCTTCCCAATTCTTGCACCTCTAACCAAGTCTTGGATGC
ATCTTCTTCTTCCCTTCTTCTTCTTCTGCTGTTTCTTCTGTTGTTTGGTGGCCACCTCTGTTTTACCCCTG
AGCTGTTTCTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTAAAGCGGATTCTCACTCTGTGGCCAGGCTG
GAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAAGCGATTCTCCTCCCCAGCCTCC
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTTTTTCCACTCTTCTTTTTTCTCAT
TCTTTTCTGGGTGCTGTGCGCTTTCTTATCTGCCGTGTTTTGCAAGCACTTCTCCTGTGTCTTGGGAGCCCT
GAGACTTCTTTCTCTTCTGCTTCCCTCCACCCACCTCCAAGGTGCTGAGCTCACATCACACCCCTTGCAGCCGCTC
ATGCCACAGCCCCCAAGGGGCCCATATGCCAAAGCATGCCGCCACCCCTCGTGTGCTTTAGTCAAGTGTGTAC
GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCCAGTGGAGGAA
GGTGTGCAGTGTACTTCCCTTTAAATTAATAAACATATATATATATATATTTGGAGGTCAAGTAAATTCGAATGG
CGGGGAGGCATTAAAGCACCGACCTGGGTCCCTAGGCCCCGCTGGCACTCAGCCTTGGCAGAGATTGGCTCCAG
AATTTTTGCCAGGTTACAGAACAACCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTTCAT
CCCAACTATTCTCTGTGGTATGAAAAAG

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FIGURE 172

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTIVTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNL
GECTNVLPPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 173

[illegible]

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FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSPSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL
SPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSYSDLSEGEQEARFAAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:
amino acids 1-15

Casein kinase II phosphorylation site.
amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328

Tyrosine kinase phosphorylation site.
amino acids 44-52

N-myristoylation site.
amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 11-22

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FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTGTTTCCCTGGCACCCCTCCTGC
TCAGTGCGACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCCTTCAGACAGGACAAC TG
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCCTTTAAAAAAAACC
AATACCAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCTATC
GGGGAGCCATGGAAGAAAATCAAGACATAAACACAACAGAACATTGCAGAAGTTTTTAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCTCCTTTGAATCTACCCACAACAGCCACGGAATAACAGATTCTCCAGTAACATCATCAGCAGA
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA
AGTGCCTTGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCCATTACAGTTAG
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAAATTCACCAATAA
TTCAAAACCTCTTTCCAAATACGTCAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTTGGGCTACTTGTTGTGTGGAAGGAAAACGGATTCAAT
TTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTCAGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTCCTATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCTATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAAAGGTTACACAAAATTACTGTCACGTGGA
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCCAAAGGTTTTT
TTTCTTACAATTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT
AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTACCATTACAGCCCTGCCTCATAACTAAATAATAAAA
ATTATTCACCAAAAAATTTCTAAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCCTACCCAGGAAAGTAATAGCTTCTTTAAAGTCTTCAAAGGTTTGGGAATTTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

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FIGURE 176

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSENFT
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFPN
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYL LCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSS
YYNPTLND SAMP ESEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

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FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCCT
GCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGCTTCAACCTGACTTTCCACCTTTCCCTA
CAAATTCGGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGG
TGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAA
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCTTCTGTGTCTCCTTACCTCAGAGG
CCAGAGCAAGCTCATTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAA
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA
CCAGGCTGAAGGTAAAAAGTTTAAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA
TTGGGACTGCTTTATATTCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
TCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTAC
TGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTACTGGGGATGGGGAGGCGAAGACGA
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAAT
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACCGAGT
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
CACAGTGGATTTCTGGTTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGAAGAAGTGAATCTTTGTTTGA
ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAAGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTT
TCCTTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAG
TCATTTTGATCATGAGGGTTAAATATTGTAATATGGTACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGA
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
TACAATACTGTTATTCAATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCAAAA
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGC
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTC
CAGTGATGCCACAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGATTTGTACAAGTAGG
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAAATATGTCTATCAAATACCTCTGTAGTAAAT
GTGAAAAAGCAAAA

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FIGURE 178

MGFNLTFLHSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLLLGKGKTLTNEASTKKVELD
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR
QQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFIHFDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR
LRYSGYFGGVTTALSREQFFKVNGFSNNYWGWGEGDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE
RMKLLHQVSRVWRDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

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FIGURE 179

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTCGAGCTCCAGCTGC
ATTCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCAATGGCCCAGGCAGTGTGGTTCGCGCCTCGG
CCGCATCCTCTGGCTTGCTGCCTCCTGCCCTGGGCCCCGGCAGGGGTGGCCGACGGCCTGTATGAACTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG
CCTGGCCCTGCCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAAGAT
GGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCCGGTCTGTCTGGGTTCAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCTCTCCCATCACAGAGTTCTCGTGGG
GGACCTTGTGTGACCCAGAACACTTCCCTACCCTGGCCAGCTCCTATCTACTAAGACCGTCTGAAAGTCTC
CTTCCTCCTCCACGACCCGAGCAACTTCTCAAGACCGCTTGTCTTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTCACCGTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGACTTCTCCGCTC
GCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGGGCCACCCTAATTCAGACCTTCCAAAAGATGAC
CGTGACCTTGAAGTCTCTGGGGAGCCCTCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGA
GGAAGGGGAGTGCCACCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGA
CTACTGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTTGCTTTCCTATGTGTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCCTCTGGGGTTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCCTTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCT
GCTCCCGCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCTCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCATTTGCGTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCCCTCCCTCTCTGTACCCCTGACCC
CAGCCATTACCCATCTGTACAGTCCAGCCACTGACATAAGCCCACTCGGTTACCACCCCTTGACCCCTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCCTGTGACTCCTAGGTGGGCCTGGCTGCCAC
TGCCCATTCCTCTCATATTGGCACATCTGTGTCCATTGGGGGTCTCAGTTTCTCCCCAGACAGCCCTACCT
GTGCCAGAGAGTAGAAAGAAGGTCAATAAGGGTTAAAAATCCATAACTAAAGTTGTACACATAGATGGGCACA
CTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACCTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAACTTTCAGTGAGGAAA
AGGCCTTGACGGGTAGAAGAGGTTGAGTCAAGGCCGGGCGGGTGGCTCACGCCTGTAATCCACGACTTTGGG
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTAACACGGTGAAACCCGCTCTACT
AAAAAATAACAAAAGTTAGCCGGGCGTGGTGGTGGGTGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCAGAACCCGGGAGGCGGAGCTTGAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA
GCGAGACTCTGTCTCA

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FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLYRFHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGFVVLPITEFLVGDLVVQTNTSLPWPS
YLTKTVLKVSFLLHDPNFKTALFLYSWDFGDGTQMVTEDSVYYNYSIIGFTTVKLKVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTNLNFGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LHTFRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAFPATLITVMLAFIMYMTLRNATQQKDMVENP
EPPSGVRCCCQCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 181

CGGACGCGTGGGCGGCGGCTGCGGAACCTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGACAGATGGCAGTGGC
CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCGGTTTCGTGGGGCCAGGGT
CCAGCGGCTGCGCAGAGGCGGGGACCCCGGCTCATGCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGG
CCTGGGCGCGCCACGGCCCGGAGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGG
CGCCGAGGAGGCGGCGGTCAGCTCCGCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGTCAG
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCTTCTGCCAGGAAAT
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGGCCTTACATGAAGACTGA
AGATGGGTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTCTACTCACCAATCTTCTCCTTGGACTCCT
CAAAAGTTCAGCTCCAGCAGGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTTTACCAG
GGAAGTAGCCCGCGCTTAGAAGGCACAAATGTACCGTCAATGTGTTGCATCCTGGTATTGTACGGACAAATCT
GGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTCAATTTGGTGTGATGGGCTTTTTTCAAACCTCC
AGTAGAAGGTGCCAGACTTCCATTTATTTGGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG
GGATTGTAAAGAGGAAGAACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGA
AGTGATGGTTGGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTTATAAACTGCATATCAGTTATATCTG
TGATCAGGAATGGTGTGGATTGAGAACTTGTACTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA
GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTGAGCAAAGATGTTTAAAT
ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAATTTATAACTGGGCAAGCA
TGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT
TTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTTGGAATTTATCTGCCTGGTGTGTGCA
CACAAGTCTTACTTGGAAATAAATTTACTGGTAC

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FIGURE 182

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELRLQAAECGPEPGVSGVGELIVRELDLASLRVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNLGHFLLTNLLLGLLKSSAPSRIVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANI
LFTRELARRLEGTNVTNVNLHFGIVRTNLGRHIHPIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK
```

Important features:**Signal peptide:**

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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FIGURE 183

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCCGAAGATTC
ACTATGGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGCACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGTATTCTGAGGATCCTGCAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGAGGATGACAACATTGCA
ATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTTGCTGGGGAACCTGCTATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCTTCGTGCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAGTAAAGAGGCAACAGATAGAGTGTCTTGGAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAATACTACTAACCCTGCAAGCTCTGTCAAATTTTAGTT
TAATTGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCCGTTGTTTTTTGTTGTTTGT
TTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTAAAT
GTTTTTGAACTTTTTGTGTAATAATATCAGATCTCAACATTGTTGGTTTCTTTTGTTCATTTTGTACAAC
TTCTTGAATTTAGAAATTACATCTTTGCAGTTCTGTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGGAATGCACAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAACCTATAATAAATTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 184

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828

<subunit 1 of 1, 263 aa, 1 stop

<MW: 29741, pI: 5.74, NX(S/T): 1

MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKEGSSGRCLTLLGLSFILAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSDPAAIHDFEKGMT
AYLDLLLGNLCYLMPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIIFYQLCNRKSF
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 185

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGGCCGCTTGCCT
CCTGCTCCTCCTCCTCGCCAGCCTGACCACTGGCTCTGTTTTCCACAACAGACGGGACAACCTTGCAGAGCT
GCAACCCACAGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCATGTTCCAGAGGCGAAGGAGCGAGACACCCA
CTTCCCCATCTGCATTTCTGCTGCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGCTAGAACCT
ACCTGCCCTGCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGGAATAAATGG
CTGGTTCTTTGTTTCCAA
AA

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FIGURE 186

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

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FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CATGTTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTCAACCT
CCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACACCAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTTCGTGGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGGAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTGGAACCTGCTGAGCAGAACCAA
TTATAACTTCCAGTACATCAGCCTTCGGCTCAGGCTCCTGTGGGGGTAGGAGTGCTGATTGCGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGCGAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGACACGGGGGACTCATGGG
TGTGATTGAGAGAGCCATGGTGAAGGCCTGCCACACGCTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCATGCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCT
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCCGCTCCTGAGCCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCGCCGCCGCCCTGCTGTGCTCTTCCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTCGCCGAGCCGACGCGGATCCCTGTGCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTTTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAG
TGAATCCCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGATGTGCTGGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAAACTGTCTGTCAGGGGCTTTCAGCAAAATGAAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTACTCCAGGCTAACCTG
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGGAATG
GTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGAAGGACACATCACGTTCA
TGTTTCAAGTACAGGCCCACAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

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FIGURE 188

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKOPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKG METIMODEVTKRFSAEELSWNLLSRTN
YNFOYISLRLTVLWGLGVLIRYCFLLPLRIALFTGISLLVVGTTVVGYLPNGRFKEEFMSKHVHLMCYRICVRL
TAIITYHDRENRP RNGGICVANHTSPIDV IILASDGYAMVGQVHGGLMGVIQ RAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLP PMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQKLYSKMIVGNH
KDRSRS

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FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCAGGCTGTTCCAC
CATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGAC
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGGAGCTCTA
CATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG
GGGCTGTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGCCCTGAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCCAACCAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTA
TGTGATGGGGACTTCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

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FIGURE 190

MALAAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSRELYMRHFFKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKT
LLLAPGEFQLSGVGP

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FIGURE 191

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACCAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCCTGCT
CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTCTGGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCAGGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACTCCCCTAAGTCTCTGCTCA

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FIGURE 192

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVSRNFSSPILARKLCEGAADDPSS
MVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENTYDTPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

FIGURE 193

[illegible]

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTPALSPTSMGPQPTTLG
GPSPTNFLLDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPPKKYVDQSDRAGGPRAF
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:
amino acids 1-25

Transmembrane domain:
amino acids 94-118

N-myristoylation site.
amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

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FIGURE 195

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA
CTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCCTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACATATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGA
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAATTTTTCATGAAATTATTCCT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 196

MKMLLLLCGLTLVCHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQIHVLENSLVVKVH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSIDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATG
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCC
TTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTTCAATAAACCCACCAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTATAGGCTATTGCTTGTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAAATGGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAAAAAAAAA

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FIGURE 198

MTCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACCNNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS
CAPPTGFNKPTSNDTMASGWRASSFHFDSSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

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FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC
TGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC
TTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

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FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCKYKSSQKQHSPVPE
KAIPLITPGSATTC

FIGURE 201

[illegible]

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FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT
REAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVPGHSGAWETSGGHGI
FGSQGGLGCGQGQGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQ
NEGCTNPPPSGSGGGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS
RGDSGSESSWGSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFQGVSSNMREISKEGNRLLGGS
GDNYRQGGSSWGSGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIIP
```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

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FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT
GGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCCAGTGTTTTCCACAGCCCCAAAACGGAACCTGGTTTTGGG
GTCACCTGGGCCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCCAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCA
ATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCTTCCATTTCAACATCCTGAAGT
CCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTCAGGAGAGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGCATGACTTCACAGACGCTGTCTATCCGGGAGCGGCTCGCACCTCCCACTCAGGGTATTGATGATTTTT
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCCTTCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCCTTTCT
CCGAGGGGCCCAGGAAGTGCATCGGGCAGGCGTTTCGCCATGGCGGAGATGAAAGTGGTCTGGCGTTGATGCTGC
TGCACTTCCGGTTCCTGCCAGACCACACTGAGCCCCGAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC
TTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCACTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATT
GTCATGAATAAAACGGTGCTGTCAA

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FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVGSWLLARILAWTYAFYNNCRRLQCFPPKRNWFWGHLGLITPTEGLK
DSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWLGEILLSGGDKWSRHRM
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLOKCIFSFDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFD DAVIRERRRTLPTQGIDDFKDKAKSKTLDFID
VLLLSKDEDEGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 205

TCCCTTGACAGGTCTGGTGGCTGGTTGCGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT
TTTGCCACAGCAGTTTCTGCGAGTTCTTTGAGGTGTGAACCCACATCCCTGCCCCAGGGCCACCTGCAGGACGC
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATC
CTCTTTGCCCTCATCACCATCCTCATCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
CGGGGCCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC
AAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGAGCAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC
CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCACCCACCACTGGCTACTCAGCTGATGTGGGC
AACAAGACCACCTACCGCGTCGTGGCCCATTCAGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTTGTCAAC
CGGACCCCTGAAACCGTGTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCCT
GTGATCCAGCGAGCGGGCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGCCGCATGCGGCAATTT
GACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCTGCTGGTTGAGCACAGGCTGGTTTACC
ATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATGGCATGGTCCCCCACTACTGCAGCCAGCGG
CCCCGCTTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGGCGGACGAATGTGTACCTACATCCAGAAT
GAGCACAGTCGAAGGGCAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTAT
GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
AGCCTCCGCCAGCCGCTAGGCCAGGGACCACTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC
AGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTGGGAGT
CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGCACTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT
TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTGAGAGCCCCAGGAATGGACCCCC
AATCACTCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACCTGGTGTGCCCCCTCAATTT
CCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCGGCCAGAGAATTTGTGGGGTGTGG
AGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
GACAAACCTTCCCCCTCTCTGGGCACCCCTTCTGCCCCACACCACTTCCAGTGCGGAGTCTGAGACCTTTCCAC
CTCCCCACAAAGTGCCCTCGGGTCTGTCTCTCCCGTCTGGACCTCCAGCCACTATCCCTTGTGGAAGGCTCA
GCTCTTTGGGGGTCTGGGGTACCTCCCCACCTCCTGGAACCTTTAGGGTATTTTTCGCAAACTCCTTCAGG
GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCCCTCAGCCAGCTGCCATTAGCTT
GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAATGTTGGAGGCGCTTTGGGG
CTGCCCCCTTGTCTGGAGTCACTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTGCTCTGGGATGGCTGTCTG
GGAGCTGTATCACCTGGGTCTGTCCCCCTGGCTCTGTATCAGGCACCTTATTAAAGCTGGGCCTCAGTGGGGTGT
GTTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGGACAGATG
GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGGGTGGGGGCGGTGACTGCCCCAGACTTGGTTTTGTA
ATGATTTGTACAGGAATAAACACACCTACGCTCCGGAIAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 206

MSSNKEQRSASFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNNKTTYRVVAHSSVFRVLRPPQEFVNRTPETVFIFWG
PPSKMQKPQGSILVRVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV
HVGMPVPPNYCSQRRLQRMPYHYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

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FIGURE 207

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGCGACGTCAC
CGCCATGGCCAGGCATCAAAGCTTTGATTAGTTTGTCTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCTCTTTGTTCTATTTTTTTTACATCCTTTACCTATTCCATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAAGTTGCCATCTTTCTTAC
AACGGGCATTGTCTGTCTAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCACTTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGGTGAAGAAATTAAGTGAATGCTCAATGGACTTCCTGTCAATTTGTTGGCC
ATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTCACAGAGACTTGCTGAAGGATTAAAGGATTTTCTCTTTTGAA
AAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT
TTCCTGTAGGTTGATTTTTTTTGAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTTGCATTGGT
TAGGAATTCAGAATTCGCCGGCTCTATTACTGGTCAAGTACATCTTTTCTTAAATTTATTTAGCCTCCATTA
TTACAAAAAATTATAAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTGTTATAGACTGTATACTCAGTGCATAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTTAA
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTGAAAATTATTTTATGG
AATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAGAATTTATGTTAACTTTAAGGTAAGGGTGTA
ACATTTTGGAGATAAGGTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG
AAATTCAGTTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATCAACCTTTCATGTTTTACC
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGCATCATATATGCCAGAAAAC
CTTCTCTGCTTCTCCTCTTTTGAATTTTGGTATGTTGTATATATTACATAAAATACTTTTCAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATTTCAGAGTGCCCCCTCCCCTGCA
AGGCTTGCCATGATTAACAAGTAAGTTAGTCTTACAGATAATTTCATGCATTAACAGTTTAAGATTTAGACC
ATGGTAATAGTAGTTCTTATTCTTAAGGTTATATCATATGTAATTTAAAGTATTTTTTAAGACAAGTTTCTGT
ATACCTCTGAAGTGTGTTTGAATTTGAGTTCATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTTGTTGTGT
GAGTTAATGCAAAGTAGCCAAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATCCCAGTAAC
CAGGCATGATCAATTTATAGTGGTCTGTTTACATCTAATAATTATCAGGACTTTTTTCAGGAGTGGGTTATAAAAA
CATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATGTTTATTCAGTATACCTACATAAAAAAT
ATTTGCGCATCAGCCAAACTCAGTAATCATGACAGCTGTCTGTTGTTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTTCACTTAAAGATGCCTAAAGCCACAGGTTTTATTGCCTAACTTAAGC
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCCTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAAGTCTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCAATCTCTGGTCTTTC
CCTATTTTCTGTTCTGGATGTGAGTGCAGTGCAGTGCAGTGTGTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTGTGCTTTGACCTTGTATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTCCATAGAATATGCACTGATACAACATTACCAT
TCTTCTATGGAAGAAAACCTTTTGATGATGAAACAATAAGATTTTAAATATCTATTTTAAAAA

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FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIFLT
T
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

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FIGURE 209

CTTGACAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCACTTGTGTTCTCTCTCCTGGTGC
AGAGTTGCAAGCAAGFTTATCAGAGTATCGCCATGAAGTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTGCTGCC
TGGGGACTTTGGGTGAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCCATTTCAGACTGGAGGGA
GAGATTCCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCGGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAAACCCTTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTCCGAGGGTGACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTATATTATGCCGCTTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAGAAACCTTCCTTTCTGGAGTTTGCAGAGTTCAG
CAATATGATAGGGAACAGGTGCTGATGGGCCCAAGAGTGACAAGCATAACAATACTATTATCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTATGAATTTCCAGTGTTCAGTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGATGATTTAGAAAAA

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FIGURE 210

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCLTGLGQAPRQKQGSGTGEFFHFQTGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQGPGRPGGNEEAKKKAWEHWCWKPQALCAFLISFFRG

Important features:**Signal peptide:**

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

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FIGURE 211

GTGCAAGGAGCCGAGGCGAGATGGGGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC
GGCGGGCCCGTTGAGTTCCCGGCGGACAAGATGGTGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATG
CTCCTGCCGCTGGATGGGGAACCTCGTCCTGGCTTCAGGAGCCGGATTGGGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCTGCCGTCTCCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG
GCCGACGTTACGCGCGACGAGGACCTGGCTGTTTCTCCTGGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGC
CGGGCGCGCTGAGCGGTGGGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 212

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR
```

Important features:**Signal peptide:**

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

FIGURE 213

[illegible]

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FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCFVCLA

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FIGURE 215

GGATTTTTGTGATCCGCGATTGCTCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAGGACAGGCCACCC
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCTTGCTTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAAGTCAACAACAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTACCCGCGAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCCCTGCCCTGGCCCCG
CAGGAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTGAGCTCCACAGGTTTCAGGTCATCATCA
TCTGCTTGGTGGTCTGGATGCCCTCCTGGTGCTTGTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCCACA
AGAATAACTATGCTGCCATGGTATTCCTACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGGTGGTCT
CATTATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTCAGAACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACT
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCTCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAATCTATAAAGATATTCTGAAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 216

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINIKKWENEEEEEEEEQPPPTPVSGEEGRAAAPDVA
PAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILDKIIQPDKNNYAAMVFHYMSITILVFF
MMEIIFKLFVFRLLSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGLLLRLRVRVARIINGIIISVKTRSE
RQLRLKQMNVLAAKIQHLEFSCSEKPLD

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FIGURE 217

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT
ATTTCCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACTTTTGAACCTGACATCAAACCTTTCTGATATCGTGATAACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGGCCGGACAGCAGTGTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTAC
CACCAGATATGACCTAGTTTTATATTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTTCATGTGAAGTACAGCAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAAGTACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAATAAACTGAGCACCTTCTTTTAAACAA
AAAAAAA

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FIGURE 218

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTSEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYMLK

FIGURE 219

[illegible]

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FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGSLLYYLTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILP
FPLQLFCFLVAIRVPFPWTVWRKTEAGVWD

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FIGURE 221

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACTTTGCCAGTGGGAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCATCCTTGGGAGAAGTCAGCTC
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCCTGTTGCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCAGTGTCCACGTGTCTGCTGAAGAACACTTTTCAATTTTGTAAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTATGAATCTAATGGAACCTCCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACA
GTGTGCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCAAGTTCTGTCTGGTGAACAAGACTCTTGGAGGAGTCATCTTTGAAAGTTTGAGTG
TGCAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCACAACGTGGGCTCCAAAGCTTCCCTCTA
CCTCTTGGCCCTTGCCAGCCTCCTTCTCGGGGACTGCTGCCCTGAGGTCTGGGGCTGCACCTTGCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTTCCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG
TTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLET
PVRLYQNMFCSAENCS
EETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGT
SCRGKPKCYEEEQCV
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTS
APTTSNHNVGSKASLYLL
ALASLLLRGLLP

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FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC
TGGCCACCCCTCCCAACCCCAAGAGCCCAGCCCCATGTTCCCCGCCGCCGGCGCGCTGCTGTGGGTCTTGCTGCTG
AATCTGGGTCCCCGGGCGGGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGCAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGGAAGGATAGCACACAGCAGAGAGCTTCCCAGTGCGACTCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCCTCA
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCACCAGTACCAGGACCACCCTACCCCCCTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTCAGTGTTCACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCTTTCAATCCTAGCAC
CCACTAGATATTTTGTAGTACAGAAAAACAAAACCTGGAAAAACACAA

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FIGURE 224

MVPAAGALLWVLLLNLGPRAGAAGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWSPSPPTAMPSPEDLRLVMPWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQLRTEHKPCTYQQPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSL
PPASPCPALAFWKVRIGLEDIWNLSLVFTEMQPIDRNQR

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FIGURE 225

CCCCGGTCGACCCACGCGTCCGGGGAGAAAGGATCGCCGGCCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCAG
CGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGGTGTACCGCGACTGCGTACTGCAGTGCGAAGAGCAGA
ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
GGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCTCAGT
TCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTTGGCTCGTTTCTCAATG
GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACACCTGTG
TGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTCTGTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
AGAAAATGGACTACTTCTGTGCCTCCACTGTATCTACACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
TGCAGCACCCAGCTGTGGTCAGTGCCTTCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA
GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTTGGCCTGGTCAACGTGGTGTGGTGGC
TGGCCTGGTGCTGTGGAACCAGCGGCGGCTGCCTCACGTGCGCAAGTGCCTGGTGGTGGTCTTGTGCTGCAGG
GGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCATCTGGCACATCA
GCACCATCCCTGTCCACGTCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
ACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCCTGCTGGCCTC
CCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTCAACTTCTTGAACCTTGGACATGAAGGATGTGGGCCAG
AATCATGTGGCCAGCCACCCCTGTGGCCCTCACAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCAGCATC
TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACCTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA
CCGGGAGGACAGCTGCCTGTTTCTCCCAACAGCCTCCTCCCAACATCCCAAGCTGCCTGGCTGGGTCTGAAG
CCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACCACCCCCA
CCCTCCTCCAGGACACCACTAGGTGGTGCTGGATGCTTGTCTTTGGCCAGCCAAGGTTACAGGCGATTCTCCCC
ATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCCA
GGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC
TGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTGTGCGGGAAGAGGTGTGGCTTCAAAG
TGTGTGTGTGAGGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGTTGGGCATGTGAGA
TGAGTGAAGTCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTACCATCAATAAT
CACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
GTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCGCCTCCTGCAAACTCACAGGGTCCCCACACAACAGTGCCC
TCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGCTGGGGCTCTCTCCATCCTCTTTTCTCCT
TGCCTTCGCATGGCTGGCCTTCCCTCCAAAACCTCCATCCCCTGCTGCCAGCCCTTTGCCATAGCCTGATTT
TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCAG
AGGGTCTTACTGTTCCAGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAGGTGACCC
CTGCCATTTACCAGCAGCCCTGGCATGTTCTTGGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTGCCCCCTGACCCCTTGTCCCTCTTTGAGGGA
GGGGAGCTATGCTAGGACTCCAACCTCAGGGAAGTGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTT
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAATCAATCCAAGCCTCAAAAAAAAAAAAAAAAAA

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FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPFSSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFWVSLNAW
FWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLMLTVHVSYSLSLIREFDYGYNI
VANVAIGLVNVVWLLAWCLWNQRRLPHVRCVNVVLLQGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFS
FLEDDSLYLLKESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 227

[illegible]

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FIGURE 228

MGAAVFFGCTFVAFGPFAFLITVAGDPLRVIIIVAGAFFWLVSLLIASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIIH
GDSPYYFLTSAFLTAAILLLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLLCKD

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FIGURE 229

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
GCCGACCCCCCGCGCAACATGTCAGCCACGGGCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC
TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCACGCCGGCGCCCCAGAG
CCTCTCCACGCTGGGCTCCCCAGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTACTACCCAGGCCTCA
CTACGCCAGGCACCCCCAAAACCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
ACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCCT
CCTACTCTGAACTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCG
TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGTGGCTACCTGA
CACTTACCTTCACCTGCAGTACCCATGGGCAGAGAGTTCCACCAAGTTCAGACACCACATGTACACCAACGTCA
GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCCATG
CATCGGACACCTTGATAAGAAGGGTCCTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA
CACTGTCCATGGGGTGTGTCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
GGGCAGTCATTGGATCTGAGTTCATCGGGATTGGTGGAAATTATGACGGGACTGGCCGGTTCCTCAGGGGCTGG
AGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
TCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGG
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCTCCCCATACCTTG
TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTGACACAGTCGGTCCCCGCAGA
GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCTAGTTCAATTCACAAGCATATGCTGAGAATAAACATGTTA
CACATGGAAAA

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTC
STPWAESSTKFRHHMYTNVSGLTSGEKKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVDDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGNYDGTGRFPQGLEDVSTY
PVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVRRESRAQSPVEAEFPYQQLSTSCHSHLVPQNGHQATHLEV
TKQPTNRPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359,
357-362, 394-399, 427-432 and 472-477.**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

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FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTGGGCAGGGCCC
GCTTTTATAGAAGCTTGATTTCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGG
AACTCGGGGCGATTGGCTGGGAAGTGTATCCACCCAAATGTACCGATTTCTTCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAAGTGGAGGCAAAGAGG
GTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTGCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCGCCCTGAGACCCTGCAGCACCA
TCTGTCTGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCC
GCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGGCC
CCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAAGCCAGACTCC
CATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCCGACCCAGCAAGATCCAG
CTGCCAGAGGATGAGTGAACAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTC
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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FIGURE 232

MAAGLFGLSARLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPEDENLYEKNPDSHG
YKDPVLDVWNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 233

GCGGCGGCTATGCGGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCTTGCGAAGCCCCA
CGCGACAGCCTGCGGGAGGAACTTGTCATCACCCCGCTGCCTTCCGGGGACGTAGCCGCCACATTCCAGTTCCGC
ACGCGCTGGGATTGCGAGCTTCAGCGGGAAGGAGTGTCCATTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCATTCACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCA
CCCTTCTGTCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT
TGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCCACACCGCTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAGTTGTATTTGATGCCTTCATCACG
GGGCAGGGAAGAAAGACTGGTCCCTCTTCCGATGTTCTCCGAACCCCTCACGGAGCCCTGCCCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACCACTACAACAGGACAACGAGACATTAGAGGTGCACCCACCCCGGACC
ACTACATATCAGGACGTATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACCTCTCGAAACCTCAACATCCAGCTCAAGTGGAGAGACCCCAAGAGAATGAGGCCCCCAGTGCCCTTC
CTGCATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCTCACC
ATCACCTCCAAGGGCAAGGAGAAACAAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC
CTCCTGGAGATGCTGATTGAGCTGCCGGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG
AAGTGGACCGAGTACAGCCAGATCCTAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCC
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGTGCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCC
CCACTCTGATTCTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGCGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGCTACAGCTGTGTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGAAATTTGAATTAAGTAACTAGAAATTCATTCTCCTCACCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGTATTGGACAGCACAGAAAAAGAT
TTCCATCACCAAGAAAGGTGGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGGATGGAGTTTACTGTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

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FIGURE 234

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELOREGVSHYRLFPAKALGQLISK
YSLRELHLSFTQGEWRTRYWGPPFLQAPSGAELWVWFQDTVTDVSKSWKELSNVLSGIFCASLNFDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKLLPCSSKAGLSVLLKADRLEHTSYHSQAVHIRPVCRNA
RCTSISWELRQTLSSVVFDAFITGQGGKDWLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPPEAEAPPVFLHAQRYVSGYGLQKGLSTLLYNTHPYR
AFPVLLLDTPWYLRLYVHTLTITSGKENKPSYIHYQPAQDRLQPHLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVLNLTPTDFSMYPYNI
CLTCTVVAVCYGSFYNNLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

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FIGURE 235

TGACGTCAGAATCACC**ATG**GCCAGCTATCCTTACCGGCAGGGCTGCCCAGGAGCTGCAGGACAAGCACAGGAGC
CCCTCCGGGTAGCTACTACCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCTGGTGGTGG
TTATGGGGGTCTGCCCCCTGGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
GATGTTCCCTCTGGAACCTCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCTATGGTCAGCCACCTCC
AAGTTCTTACGGTGCCAGCAGCCTGGGCTTTATGGACAGGGTGCGCCCCCTCCCAATGTGGATCCTGAGGCCA
CTCCTGGTTCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTTCCAGCAGTATGACCG
GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAAATGGGCTACAACCTGAGCCCCA
GTTACCCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
CAGCTTCGAGGACTTCGTCAACATGACAGCTTCTCGGATGCTAT**TG**ACCCAACCATCTGTGGAGAGTGGAGTGCAC
CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCATCATAGCCACCAAAATAGTGAGG
ACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC
AGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCCTTGTAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
TGATGCCAGTGGTGAAGTGTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC
GAGCCCATTTTCTCCAAAGTGGAATCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAATTTGCATTTTTTTTTCATTGGGGCCAAAAG
TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAACTCTGA

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FIGURE 236

MASYPYRQGCPGAAGQAPGAPPSSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVSDHSGYISMKELKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

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FIGURE 237

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATCTCCCAGGCCT
CTTTGCCCCGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACCAACTTGCCCTCAGCTCGGACA
ACCTTCCCTCCACTGGCCCCCTAACTCTGAACATCCGCAGCCCGCTCTGGACCCTAGGTCTAATGACTTGGCAAG
GGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATGGCTTCCCACCTGCAGGAGGTTCCTGCAGTGCAGAGGTGGCC
TCCATCGTGGGGGCTGCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGA
GGACCGCCTGGGGGAAGCGCTGCCTGAAGAATCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGG
CCCTTTGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGACTCGGA
GTCCAGACGACTGCCCCGTTCTAATTCACTGGGAGCCGGGGGAAAAATCCTTTCCCAACGCCCTCCCTGGTCTCT
CATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTGTGTCTGGGGAGGTGGAGGCCCTGG
GACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGAATCTGGGGTATCAATAATCAACCCCCAGGTACCAG
CTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAA
TATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATAACCAGGTATCAATAACCCATTTCCTCCTGG
AGTTCTCCGCCCTCCTGGCTCTTCTTGGAACATCCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTCAGTG
GGGCTTAGAGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCCTGCTGTGTGGGCTCA
ATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCACTTTTCAGTGCCTCCCCTGCTCATCTCCAATAAAATA
AAAGCACTTATGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 238

MQGRVAGSCAPLG LLLVCLHLPGLFARSIGVVEEKV SQNFGTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRLPRNSNLGAGGKILSRPPWSLIHRVLPDHPWGTLPNPSVSWGGGGPGT
GWGTRMPHPPEGIWGINNQPPGTSGWGNINRYPGGSWGNIINRYPGGSWGNIINRYPGGSWGNIHLYPGINNPFPFPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-
274, 270-275, 280-285, 281-286, 305-310

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FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCG
CTGCTACCGCGTCTGCTGGACGCGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCCGAGAGCTCAAGCGCCC
AGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCT
GGGTGGTGTCATCCCCTTGGGGCTGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCT
CTTAGAGGAGCTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCAGGGAGGA
CAAGGAGGAGATCCTCATGCTGCACAACAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGGTGGGGCCTGGGCCACCAGCCTGCTCTGTTCCCCAG
CCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTG
TTCTGTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCA
TGCCCTGAAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAGGCATGC
ACCATGGTGCCCGAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
CTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCCTGTCTGG
CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACACGTGGGTCCCTGTGCAGAGCCTGCCTCGTTGCCTTC
ATGTCACCTCTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCC
AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTCCTTAGCCCG
TGTGAGCCTCACTTTCCACTTGGAGAGTCCCTCCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAGGAGCTAACGGTGACAGA
AGACAGCCAAGGTCAACCCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCATGCTGCTACTTGAC
CCCAAGCTCCAGTGTGGAACTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCAG
GGTCCCTCCTCGTCCACCAACCGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTTTTAAACAAACC
CACGTCCCAGCCTGGGTAAACATGGTAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGC
TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGAC
CCTGTCTCAAAAA

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FIGURE 240

MSCVLGGVPIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ
WHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCA
TTGAAGCCTGTGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCCACCCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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FIGURE 242

MSGGLPIVLLLTLLGSSHGTGPGMTLQKLKESFTNSSYESSFELLEKLCLLLHLPSTSVTLHHARSQHHVVCNT

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FIGURE 243

GGCAAGTGGAACCACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT
AACTGTCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCCTTTATGGATCC
ATTAAAGCTTCTTCTGAAAACCTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

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FIGURE 244

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855  
<subunit 1 of 1, 93 aa, 1 stop  
<MW: 10161, pI: 7.39, NX(S/T): 0  
MKLVTIFLLVTISLCSYSATAFLINKVPLPVVDKLAFLPLDNILPFMDPLKLLKTLGISV  
EHLVEGLRRCVNELGPEASEAVKKLLEALSHLV
```

Important features:

Signal peptide:

Amino acids 1-18

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FIGURE 245

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTTTGCTGGTGCCCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGA
GCCCATGCCAGTGCCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT
GCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCCAACCCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTTCTCCCTAACTTTAGAAATG
TTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT
GAAGGGAGGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTTCGAGGCGGCCCTCAGGAGTGGATGCGATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTC
TTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTTCAGCATGTGTTCCCTTCTGCAGTGGTCTTATC
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGAAGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCTCACCTGCACCTGAGGGGTCTGGGCAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA
ACACCACAGCCCTGTACTTGGGTTCCTCTTGTCCCTGAACTTCGTTGTACCACTGCATGGAGAGAAAATTTTG
TCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTCTCTCA

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FIGURE 246

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIVIIYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

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FIGURE 247

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTTCAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTG
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG
TTCCCTCCCTCCGATTGTTCTAAATAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAAATAGAAACCTGTGTTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTATGTGTGTTCTTGGCTGTATTCATAAATTATATATTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTACAGTACTGTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

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FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 249

AGCGGGTCTCGCTTGGGTTCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCGCGACCCAAGTGAGGGGCCCCGTGTTGGGGTCTCC
TCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCTGCGGACCCCTCGCCGGGAGATGCGCGGTGATG
CGGAGCAAGGATTCGTCTGCTGCCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTGGCGGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTACATATAAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAA
CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACAACGCAAGAAGGGTTCTCATGGGCTGAAAATTTCCAGCGT
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG
TGTCAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
CATGGTGGAAAATAAGGTTGAGATGCAGAAGATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
AAAGGGAGAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAAATAATGTACACATTTGTGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAAT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC
TTATACAAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA
TACAATAGGTTCTAAAATAAAAATTGCTAAACAAGAAATGAAAACATGGAGCATTGTTAATTTACAACAGAAAAT
TACCTTTTGATTTGTAACTACTTCTGCTGTTCAATCAAGAGTCTTGGTAGATAAGAAAAAATCAGTCAATAT
TTCCAAATAAATTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCTTTAGGAAGACAAATAAATAACAAACAACAG
CCACAAATACTTTTTTTTCAAAATTTTAGTTTTACCTGTAATTAATAAGAACTGATACAAGACAAAAACAGTTCC
TTCAGATTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTCTGCTCTGAATGCATTATATTTTCCA
AACTATACCCATAAATTGTGACTAGTAAATACTTACACAGAGCAGAAATTTTACAGATGGCAAAAAAATTTAAA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
GATAGAATTAGATTGGTAAATACATGTATTCATACACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTTGGGAAAACTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
CATAATATTTACTATGCAGATGAATTGAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTTATTTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTAGGAGGTTTACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGCTAGTTTCGGTTTTCTGCAGCCATTGGCGTTAAAAAATATAAGTAGGATAACTTGTAAA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG
TAGACCACAATTCATTTTGTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAATAATTTCAACTTCCCATATATTTACTAAGATGATTAAGACTTA
CATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGGTTTGTATAAACAGGT
TGCTATAAGCTTGTGAATGAAATGGAACATTCAATCAAACATTTCCTATATAACAATTATTATTTACAAT
TTGGTTTCTGCAATATTTTCTTATGTCCACCCTTTTAAAAATTATTATTGAAGTAATTTATTTACAGGAAATG
TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAATTTTCTCCTCTAAAACTGAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 250

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQGSSACMVCRRKKRCHRDGMCCPSTRCNNGICIPVTESILTPHIPALDGTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

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FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTTGGGATTAC
AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
CTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAAT
ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTTAACATACTTGTG
AAAATACTTGATGTGTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCTTTT
AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAAATGGCAAACATCACCAGCTCCAGAT
TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
CCCTACAACCTACTACTTCTTGGGACCTCAAGCCCCAACATCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAA
ATCTCAACCTGAGCCATCCCGAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT
TCCTCCTCCTGGTTTGGAGTCCTTTCCCTTCCAGGCCAAAACCTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
TGTGAACAAGCTTTTGCAGCTTCCCAGCAGCACCATTGAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
ACACATCAAACCTTGCTAAGCGCGGATACCCCCAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
AGCAGATGTCACAGGATTAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGG
ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTCCCATCAGCTTGTATTCGAAGTCTTTAAGTGAGCCTTTGAA
TACATCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTGCAGTCTGAC
AAGCTCATCACTGAATCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAACAGAGGAAGAG
GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTGCTTAAAAAGCAGCCCTTTTGCCTTTTTTG
TTTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAGGAGGTGGTGGTCTCATA
TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
GTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCCAAAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACC
ACCTTGGGCAACATGGTGAAACTCTGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCC
TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
CTGAAAAGA

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FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPPPGLESFPSQAKLRESTPGDSPSTVNK
LLQLPSTTIENISVSVHQPPQPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSENSNOIPIISLYSKSLSEPLNTSLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQ
SPVSSSESAPGTIMNGHGGGRSQOTLDSKYSSKLLLSWLVPKQKRIAHVMWKTTPVGQWLIR

Signal peptide:
amino acids 1-24

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FIGURE 253

GGGCGCCCGCTACTACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGATGTCGGAGCTCAT
GGGGCTGTGGTGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGCTAGCGGGGGGTGGCTGCGCGCGGG
GGAGGAGAGGAGCGGCCGGCCCGCTGCCAAAAGCAAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAA
GCAGAAACAATATCAGCGGATTCGGAAGGAGAAGCCTCAACAACACAACCTTCACCCACCGCCTCCTGGCTGCAGC
TCTGAAGAGCCACAGCGGGAACATATCTTGATGGACTTTAGCAGCAATGGCAAATACCTGGCTACCTGTGCAGA
TGATCGCACCATCCGCATCTGGAGCACCAGGACTTCCTGCAGCGAGAGCACCGCAGCATGAGAGCCAACGTGGA
GCTGGACCACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCCTTCATCGTCTGGCTGGCCAACGGGGACAC
CCTCCGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGGTACACCTTCACAGCCACCCAGAGGACTTCCCTAA
AAAGCACAAAGGCGCTGTCTATCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACAC
CACTGTCTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACACACACGC
TGCTGTATCTCCCTGTGGCAGATTTGTAGCCTCGTGTGGCTTCACCCAGATGTGAAGTTTGGGAAGTCTGCTT
TGGAAAGAAGGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAACATAAGGGCCACTCCGCGCTGTGCACTCGTT
TGCTTTCTCAACGACTCACGGAGGATGGCTTCTGTCTCAAGGATGGTACATGGAAGTGTGGGACACAGATGT
GGAATACAAGAAGAGCAGGACCCCTACTTGCTGAAGACAGCCGCTTTGAAGAGGCGGGGTGCCGCGCCGTG
CCGCTGGCCCTCTCCCCAACGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCATCTCTACAATACCCG
GCGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCCAACCTTGTCCTTTGACATCACTGG
CCGCTTTCTGGCTCCTGTGGGGACCGGGCGGTGCGCTGTTTCAACAACACTCCTGGCCACCGAGCCATGGTGA
GGAGATGCAGGGCCACCTGAAGCGGGCTCCAACGAGAGCACCCGCCAGAGGCTGCAGCAGCAGCTGACCCAGGC
CCAAGAGACCCTGAAGAGCCTGGGTGCCCTGAAGAAGTAGTACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGA
GGGATCTGGCTCCTCATGGCACTGCTGCCATCTTTCTCCAGGTGGAAGCCTTCAGAAGGAGTCTCCTGGTT
TTCTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTTAGGTCTCTCTCTTCTGCTGGCTGT
GACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTCTCCAGGCCAGTGGGTGGAATCTGTCCCACTGGC
ACTGAGGAGAATGGTAGAGAGGAGAGGAGAGAGAGAATGTGATTTTTGGCCTTGTGGCAGCATCCTCAC
ACCCAAAGAAGTTTGTAAATGTTCCAGAACAACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTGTCAAGGATG
GGAGACTGGGATAGCTTCCCATCACAGAAGTGTGTTCCATCAAAAAGACACTAAGGGATTTCCTTCTGGGCCTCA
GTTCTATTTGTAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCAAAGATGATATGAGGCTAAGAGAATATCA
AGTCCCCAGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTCATGAAAGTGGTAAAAGTGGGAA
CCAGTGTGCTTTGAAACCAATTAGAAACACATTCCCTGGGAAGGCAAAGTTTCTGGGACTTGATCATACATTT
TATATGGTTGGGACTTCTCTCTTCGGGAGATGATATCTTGTAAAGGAGACCTCTTTTCAAGTTCATCAAGTTCAT
CAGATATTTGAGTGCCCACTCTGTGCCCAAATAAATATGAGCTGGGGATTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQIRKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFS PDCRA
FIVWLANGDTLRVFKMTKREDGGYTFATPEDFPKHKAPVIDIGIANTGKFIMTASSD TT VLIWSLKGQVLSTI
NTNQMNNTHAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQAQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

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FIGURE 255

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCCCTTCTCGGCGCTGCCAACCC
GCCACCCAGCCC**ATG**GCGGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCCGCTGG
GGCCGAGCCTGGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC
CTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGGCACCTACCGGCCCAGT
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG
CCCATCT**TAG**GTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 256

MANPGLGILLALGLPFLLARWGRAWGQIQTTSANENSTVLPSSSTSSSDGNLRPEAITAIIVVFSLLAALLAVG
LALLVRKLRKQRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 257

[illegible]

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FIGURE 258

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTYLFEATEKRFFFKN
VSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMQSIDSVVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL
KISQRIVCLVLDKSGSMGGKDRNLNRMNQAAKHFLQLTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGENTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKM
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNDGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTLEDFSRASGGAFFVVSQVPSLPLP
DQYPPSQITDLDATVHEDKIILTWAPGDNFDVGKVQRYIIRISASILDRLDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:
amino acids 1-21

Putative transmembrane domains:
amino acids 284-300, 617-633

Leucine zipper pattern.
amino acids 469-491, 476-498

N-glycosylation site.
amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

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FIGURE 259

CGCCGGAGGCGAGCGGGCGCGTGGCGCAGCGGGCAGACTGGCCGTTGTCTCAGAGGACGACTTTTCAGCACAGTTCAA
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC
CGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
GTCTACTGCCATGGAACCTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG
CCACCGGGGAGGACCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC
CCTCCATGCTGTGCCTGGTGGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTTGCTTGGCCTCAC
TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGGTGGACACTTCTCCTGGACCCGTGGTT
TTTTTGCGGTCAACATTGTCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA
TGACCGGCTCCTTTTCTATGAGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA
TCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCTG
TTCTTGCGGCCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCGGTGGCCTCCA
GATTCATTGATTTCCACACACCCCTCTCCGCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCT
ACGCTTCTTCATCACCAGCCTCATCTACCCCGCCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
CACTGTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACTTTGCTGACCTATGTGGCCGGC
AGCTCACCAGCCTGGATCCAGGTGCCAGGGCCCCAACAGCAAGGCGCTCCAGGGTTCTGCTCCTCCGGACCTGCC
TCATCCCCCTCTTCTGTGCTCTGTAACACCAGCCCCGCTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
ACCCCGCACTCCTCAGCTCCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCCTGGCCCTCCTCTACGGGCCTA
AGATTGTGCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCCTTTATGTGTGCTTGGGCTTAACACTGG
GCTCAGCCTGCTCTACCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTGGTGCTTCAGAGCCTT
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCCTAAAGTTTCACTTGGGGACAGAGAG
CAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCGGTGCAAGGCAGATA
TTCCAGTCATATTAACAGAACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA
GCTGATGGTTAAACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACAAA
GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCCAGCTGACAGCGAGATGCAA
GCAAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCCTGGCATGGTCAGTCCTCAGGC
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACTGCCCCTAACCCAGACTGGAAAACCCAG
AAAGATGGGCCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCT
GGCCTGGGTTTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAA

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FIGURE 260

MAVSEDDFQHSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGIGSLLPWNFFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAI FMVIT
ALVKVDTSSWTRGFFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLA AHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VVMSEFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

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FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAAGCTGGAAAGCCCACTCTCTTGGAAACCACCACACCTGTTTAA
AAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGAAGTGTGGGTGCTGGCCTTCTCTGTGGAAGTGTCTCT
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA
CACACAGCTGCATGCCTATATTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACAGATTGG
TAACTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGG
TCTGGTTGTCCATGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCATGGTGACATA
CTTAGGACTGAGTAAGAGCAGTAAAGAGCCCTTTAGAGGTGAACGCCACGGGAGTGGCCATGCTTTCTCTGC
CGGGACATTTCTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCACAGCCACAAGCCCGA
TGCCACGGGAGGGAGAGGCCCTCAGCCGCTGGAAGTGGCAGCCCTGGTCTGGGTTGCCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGGCATCCAGTGAGAACAGC
CGGCACGTGACAGCTACTCACTTCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCCTAGAGTCCA
GAGGGGAGGTGAGGTAAACCTGAGTAATGGAAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTA
TAGACATCCCATTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCCTTTAATATTTCTCTTAACCTTATTCTC
AGGGAAGATGGAATTTAGTTTTAAAGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAAATAC
AGTGTTCGTAAATTAAGCTATGTCTCTTCTCTTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTAAACA
TGGTTCACCATGTAAGACTGGTGTCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATAGCACCCACTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGTCAGGAAAATGATAGCAAGACACATGAAAGCTC
TCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTAAACAGCTCCTTTGGCACGTGCCT
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCTAGAGAGGAGCCAAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTT
TAAGTGATTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAATGTATGGTTGTCC
TTTTTTTTTGTTTTTTTTTTTTTTAAATATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCCT
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTCTTTGCTTTTCTTAACCTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTGTGTGGGATGAATCTTATCAGGACAA
CCACTTCTCGAAGTGAATAATGAAGATAATAATATCTTTATCTTTATCCCCCTTCAAAGAAATTACCTTTGTG
TCAAATGCCGCTTGTGAGCCCTTAAATACCACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGTTAACAGACTAGGATAATTTTTTTTTCATATTTGCCAAAATTTTGTAA
ACCCTGTCTGTGCAAAATAAGTGTATAATATTGATTATTAATTTATTTTACTTTCTATACCATTTCAAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTGTAAACGTTTCTATGAC
GCATAAGCTAGCATGCCTATGATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAAGCTT
GTGAGCCCTCTGTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATAACAATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCTTCAAAACTATATGTTGCTTAGATTCTCTCTGGAAACTGAC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

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FIGURE 262

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQIGNSHVHSTDDPEAARSSNSKITTTL
GLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKLLVFALAAPVMSMVT
YLGLSKSSKEALSEVNATGVAMLFSAAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:
amino acids 1-18

Transmembrane domain:
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 263

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAAGACCGGGAAAGACCATACGTCCCCGG
GCAGGGGTGACAAACAGGTGTCTATCTTTTTGATCTCGTGTGTGGCTGCCTTCCTATTTCAAGGAAAGAC
GCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCC
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACTTGTGG
TTGGAGGAGAGAACCTTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG
GACCAGAAGAAAGGAAAGGTCCCCTCTTGCTGTTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA
GGTGAAAACCTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAGTAGAGA
AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAAGACTCGTTCTAGAAGGAAATGGATGCAAGCAGC
TCCGGGGGGCCCCAAACGCATGCTTCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCT
TTGAGGGATGCCACCGGTTCTGGACGCATGGCTGATTCTGAATGATGATGGTTCCGCCGGGGGGCTGCT
TGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCTGCTGTGCTATCTCTGTCTGTACATGT
TGGCTGCACCCCCAAAAGGTGACGAGGAGCAGCTGGCACTGCCAGGGCCAAACAGCCCCACGGGGGAAAG
GAGGGGTACCAGCCGCTCCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGAGCAGCCTGAAGCG
GCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGGAGTGAGCAGCTCAGGAATGGGCAGTACCAAG
CCAGCGATGCTGTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGGCCGACCTCCTGGCC
TTCTGCACCTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGC
AGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCG
AGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGGAAGCCATTGAATCAGCTTGGAGACC
CTGAACAATCCTGCAGAGAACAGCCCCAATCACCCTCCTTACACGGCCTCTGATTTTCATAGAAGGGAT
CTACCGAAGAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAAT
TCAAACGGCTCATCTTATTTGACCAATTCAGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATG
GCCAACACGCTTATCAATGTTATCGTGCCCTTAGCAAAAAGGGTGGACAAGTTCCGGCAGTTTCATGCA
GAATTTCAAGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAG
AAGAAATAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTTACC
TTCTCCAGCTGAATGGAGAATTTTCTCGGGAAAGGGACTTGATGTTGGAGCCGCTTCTGGAAGGG
AAGCAACGTCCTTCTCTTTTTCTGTGATGTGGACATCTACTTCACATCTGAATTCCTCAATACGTGTA
GGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTTCCTTTTTCAGTCAGTACAATCCTGGCATA
ATATACGGCCACCATGATGCAGTCCCTCCCTTGAACAGCAGCTGGTCATAAAGAAGGAACTGGATT
TTGGAGAGACTTTGGATTTGGGATGACGTGTGAGTATCGGTTCAGACTTCATCAATATAGGTGGGTTTG
ATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC
ATAGTGGTACGGACGCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAGCT
GACCCCCGAGCAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCCACGGCCAGCTGG
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAAAACAGAAACAGAAGACAAGTAGCAAA
AAAACATGAACCTCCAGAGAAGGATTGTGGGAGACACTTTTTCTTTCTTTTTCGCAATTACTGAAAGTG
GCTGCAACAGAGAAAAGACTTCCATAAAGGACGACAAAAGAATTGGACTGATGGGTCCAGAGATGAGAA
AGCCTCCGATTTCTCTCTGTTGGGCTTTTTTACACAGAAATCAAATCTCCGCTTTGCGTGCAAAAGT
AACCCAGTTGCACCCCTGTGAAGTGTCTGACAAAGGCAGAAATGCTTGTGAGATTATAAGCCTAATGGTG
TGGAGGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATG
ATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA
TTATGATACTAGTGAGTACATTAAGTAAAAATAAATGGACCAGAAAAGAAAAGAAACATAAATATCG
TGTCATATTTTCCCAAGATTAAACAAAAATAATCTGCTTATCTTTTTGGTTGTCTTTTAACTGTCT
CCGTTTTTTTTCTTTTATTTAAAAATGCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA
CCACTTTGCAAGCCTTACAAGAGAGCACAGTTGGCCTACATTTTTTATATTTTTTAAGAAGATACTTT
GAGATGCATTATGAGAACTTTCAGTTCAAAGCATCAAATTGATGCCATATCCAAGGACATGCCAAATG
CTGATTCTGTGAGGCACCTGAATGTGAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGA
CGTACAGATACTTTCTCTGAAGAGTATTTTCAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG
ACACTTTCTGCTTTACAGAAAAGGAAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAG
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAGTATACCGT
GTGAACCAAAACATCTCTTTCAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATG
GAGAAAAATATATATATATATATATATATATTGTAAGAGTCAATCCATCTGCCAGAATCTAGTGGGATG
GAAGTTTTTGCTACATGTTATCCACCCAGGCCAGGTGGAAGTAAGTGAATTTTTTTAAATTAAGC
AGTTCTACTCAATCACCAAGATGCTTCTGAAAATGCAATTTTATTACCAATTTCAACTTTTTTAA
AATAAATACAGTTAACATAGAGTGGTTTTCTTCATTGATGTGAAAATTATTAGCCAGCACCAGATGCAT
GAGCTAATTTCTCTTTGAGTCTTGGCTTCTGTTGCTCACAGTAAACTCATTTGTTTTAAAGCTTCAA
GAACATTTCAAGCTGTTGTTGTTTAAAAAATGCATTTGATTTGTTGTTGTTGTTGTTGTTGTTGTTG
AATTAACACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAATATGATTTGTGGATATGAA

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FIGURE 264

MMVVRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNIVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYE
LTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNT
QPGKKVFYPVLFSSQYNPGIYYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDLKGGWGGED
VHLYRKYLHSNLIIVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

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FIGURE 265

GGATGCGAGAAAGCCTCAGTGTGCTCTTCTGCGCTGGGCTGCTTCTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGGAACCTGGGGCTGCTGGATGGCTTCCCGATTTTCGCGGGTGTGTGGTGCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCTGTCTCCCTACCCCT
TCTTGGGCAAACCTAAGCTCCTTGCAGAGGATCCTGGAGATTAGCCCCACCATGCCCGCTCTACCGATCTCAGG
TTGACCTCTACCAACCATGCAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG
GTAGTAACCTTCGCCAGCCACGCCATAGTGGAAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTCTTCTTCCCATCCTTCA
ATGTGAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGGCCA
AGAACTTAGCCAGATGGACAGGTGATCCAGGGACTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCAATGGAGTACCACAAATGGAGACCATGGAGGGACAGTGGAGGTCTCAGCTGCTCTCTTTCT
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCTGCCATCCATTTGGGAATATCGGGGAAGTATGGCTGAGCTATTCTCAG
GGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCGATTTCTTACACTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCAAGCCCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCCAAGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATTCTGCCTCTACTCCTGACACCTGTGGCCTGGGGCTGGTTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAAGCTCATTCCTCCCTT
TTCTGGGAAGCCCTGGCTGGCTGGGGTCCAAGAGGCCCTGGCAACCTGTTTCCCATCCCTGGGCGGCTCC
TGTTACTCCTGCTGTTTCTGCTTGGCTGTGTTCTTCTCTGATAGTTTGTGTAGCTGAGGCGAGGCGACCCCT
TCCTTTTGGGCTCATTATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGCCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
CGCGCTGGTGGCCCTGTAGCTGCCGTGCCCTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTGGGGG
CAGATGAGGCTCCCCCGCTCTCGGGCTCCTGGTCTCTGGGGCATCCATGGTGTGCTCGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGTTAGAGAGGACCAATCTCAGGGTCCCCGACTGTGGCTG
CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTACAGCCCTCACCCTGTTGGCCTTCCCACTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCCCTTCTCTACATCTGCTTGCTG
CTGGGATACCCGTCAACACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCCATGGCCA
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTTCCAGCCATCCATTGGCATGCAGCCTTCTGTGGGATTCC
CAGAGGGTCTGGCTCCTGTACTTGGCTGCCTGCTTTGCTAGTGGGAGCCAAACACCTTTGCCTCCCACTCTCT
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAAGCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCTCAAGTACCTCTTTATCCTTGGTATTTCAGATT
TGGCCTGTGCTTGGCAGCCTCCATCCTTGCAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTCATAT
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTCAAGACCACAGTGGAGTA
TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGGGGCTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGAATTGCACTATAATCCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAGTGAATAAAATGATAATAT

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FIGURE 266

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQKPGACWMASRFSRVVLVLI
DALRFDFAQPOHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQVDPPTTTMQRLKALTGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLFPGAFSKAFFFPSEFNVRDLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGHPEMAKKLSQMDQVIQGLVERLENDTLVVAGDHGMTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPOVSLVPTLALLLGLPIPFNGIGEVMAELEFSGGEDSQPHSSALAAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAETLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFCILLASQWAI SPGFPFCPLLLTPVAGLVGAIYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVLLLLLFRLLAVFFSDSFVVAEARATPFLGSGFILLLVQLHWEGQLLPKLL
TMPRLGTSATTNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWLRLRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMLPRAVAGL
AASGLALLLWKFPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGRLERTKSQGPLTVAA
YQLGSVYSAMVTALTLLAFPLLLLHAERISLVFLLFLQSFLLLHLAAGIPVTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVFPAIHWHAFAFVGFPFEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQOP
PGNEADARVRPEEEEEPLMEMRLRDAPQHFYAALLQLGLKYLFI LGIQLACALAASILRRHLMVWKVFAPKFI F
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,
1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

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FIGURE 267

[illegible]

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FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPAASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE
PLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPCYQSV
LWTVFYRRSQISMEQLEKLGTLFSTEEPSKLLVQNYRALQLNQRMVVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

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FIGURE 269

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGGACTTTCTCCTG
GGGAACCCGTTTCAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCGCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCCTGGGGCTGACGCGTTCCGCAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCCATGACTGAC
CTGGACATGCTGTCACCCATCCACACACCCAGAGGACCGTGTTCAACTCAGAGACACAATCAGGACAGGATTCTG
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCGCCCCGCCATACTCTCCG
GTGACACGCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG
TGAGGGTGATGTCGGAGATGCTGACGGAGCTGGTGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCCTGAGTGATACCCTGCTCCGGGGCCCATGCCCAAGGA
GCCCTTCAGAGCCCACACTGCCAGTCGAGGCCCTGGCTGGAGGCTGGCCACAGTGGAATTTCTGCCGAGCCTATTG
TCCCTACCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGGCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCCCTCCGCTGCCTTGCCCTCCATCCTTCTCTGT
TCCTTCTGGCCGGGCACACAGCACTGGGGCTCACCTCTTGTTGATCCTCTTGTAAGTGGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

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FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGRHFHVLVASQDFVESVLVRTILPKNNPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLE
FPMTDLMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

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FIGURE 271

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCGTGAAGCCCCCGCAG
GCTCCTGGGGGGCCCAGATCATCGGGGGCCACGAGGTGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC
TGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGAACCGGG
CTCACGGCTCGTTTTCTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCCCCAGCCCGGCCCTGCTGGGACCACCAGGC
CCCCAGGAGAAGCCGCCTGAGCCACAACCTTGCGGCATGCAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAGGGGCAGAAGCAAACCCAGTAAATGTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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FIGURE 272

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRLPGRRARP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKHLLTLMCTRS GDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:
amino acids 1-30

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FIGURE 273

GAAGTTCGCGAGCGCTGGCTATGGGTCCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCG
AGCGCCGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCA
AACGCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTTTAGAGAGTCACTGGCTCTGCCATCACTG
ACCTGTACAGCCCCAAACGGCTCTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCTATGACA
TGGGGGATTATTACCATGCCATTCATGGCTGGAGGAGGCTGTGCTCTTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTCTCTACAGCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGTTGGTAGCTGAGGCTGTCTCCAGAGGCCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTGACACCCTGGGTTCCAGCCCACTCTCTACCAGATCCCTA
GCCTCTACTGTTCTTATGAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCTCCACC
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTGCTGACTCAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC
CATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAAGTGCCT
GGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCTCAACCACCGCATTGCTGCCCTCACAGGCCCTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG
CTACGTCACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTCGCAAATCAGAGGCAA
GGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAGGAGGGGGAGTGGAGCCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCAAGCAGGGAGTGTCCCCCTCCAGAAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA
GTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTAAACACAGTCATAAAAATGTTTATAAATCAAAA

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FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARIAALLAVLALGTGDPERAAARGDTFSALTSSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLT
GDDCFQVGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMAVNLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDT
YEGLCQTLGSOPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP
PYAEYLQVVNYGIGGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSS
SPED
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

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FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCAGCCACACATCCAGATTAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATCAAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAAACGTGTCTCTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATAC
ATATGCGAGTTCACCATCCCTAAATAGGCTCTTTCTCCAATGTGTCTCCCAAGCAAGATTTCATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTACTTATTAATAAATTTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCTTCTGGGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAACTTTCTCTCTAGTCTTTC
TCACTTGTACAAACCCAGTTTGTCTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTGCTCATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
CATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTCTGATTTGATTTTCTTCTCATGCCTACCCTTTTGGAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTGATCAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCCTTTTTTACATTTTCGTATATTTAT
TTTTTTTAGCCATCATTTATATGTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAACCTGAATTTAAAG
AATGCTATCTTGGAAAATTGCATACGTCTGTGCAATTTTATTTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTGTAGAAG
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTAAACATTGAATGTGTTTGTGAACAATATCC
CACTTTCAAAACCTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTCATTGCTCAATAATAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHSRKARKHSKRRVRDKDGLKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKE
VDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGKWSDEACRSSKRYICEFTIPK

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FIGURE 277

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCCCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCTTCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTATGTTTCATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCCTGAACGACAACATTGGAAGAGGAATTGAGAATACT
ATGATGATCTGGACTTCAAAAACATCATGGACTTGTTCAGAAAAAGTTCAAGTGTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCCCTGGACCCCTGGCCTGTGGGGTGCCTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAATATCGACAAGGAGCGTTTCAGTGTGC
AGGATGTCATCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGTTTCATGGACAACATACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTCCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCGTGCCAAGCCCAGCCTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGCCCGAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGGCCCTCTGCCACACTCAGTACTGACCAAGCCAGG
GCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTCCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGC
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGGGCATCTGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCCAGGTGCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCCCTTGAGCCTAGTTTTTTTTTACGTGATTTTGTAAACATTCATTTTTT
GTACAGATAACAGGAGTTTTCTGACTAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAAC
CAGTTTGTAAATCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

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FIGURE 278

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIIYAEVERQKYKTLES AFLAPAILILLGVVMFM
VSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRGIIENYYDDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTYTCIRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN

Signal peptide:
amino acids 1-44

Transmembrane domains:
amino acids 22-42, 57-85, 93-116, 230-257

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FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTCACCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCTGAAGCACATCATCTGGCTGAAGGTCAACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC
CCGCCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAAGTGTGTATAAGCTCTCCTTCCT
GGTGAACGCCTTAGCTAAGCAGGTCAAGACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTCAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGGA
CAACATCCCGTTTCAAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCTGTGGACTCTGTGCTTCCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAAGTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGT
GAAGGCCTTGGGATTCGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCTGTGAAAA

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FIGURE 280

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFITLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILOQLPLLSAMREKPAGGIPVLGS
LVNTVLKHHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIVEFHMTTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPAIKGDITQLYLGAKLDSQGVTKWFNNSAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPE
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAQFYTKGDQLILNLNLISSDRIQLMNSGIGWFQPDVLKNIITEIHSILLPNQNGKLRSGVPVSL
VKALGFEEAAESSLTKDALVLTPASLWKPSSPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

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FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCCGCGTTCT
CTTTCCACCTTTTCTCTTCTTCCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTGCCACCGCTGCTTCCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTTGATCTGTGCCCTGTGCCCTCCGTGTC
CTTTTCGTCTCCCTTCTCCCGACTCCGCTCCCGGACCAGCGGCCCTGACCCTGGGGAAAGGATGGTTCCCGAGGT
GAGGGTCTCTCCTCCTTGTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGA
CATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCTACTTGGAGCCACAAGGCCT
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCCCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTG
CCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGCCCGGGCACCCCAAGCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAAGTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTGCCCTGCATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCCGTACCCCGAGAA
AGTGGCTGGGAAGTGCTGCAAGATTTGCCCAGAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGTCTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTC
CCTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGAAGTCAAGAAAGTCAAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCCTAG
CCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCTCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLGLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFPSRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGPPTPAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSDPGAEHGQSRQSDQDITKT
```

Signal peptide:
amino acids 1-25

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FIGURE 283

CGCATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTTCGGATTGCAACGAGGAGAAGAT
GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
GCCTCGCCCTGTTGTGCTGCGCCGCGCCGCGCCGCGCGTCCGCTCAGCCGCCTCGGCGGGGAATGTCACCGGTG
GCGGCGGGGCGCGGGGCGAGGTGGACGCGTCGCCGGGCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTA
GGGCGACGGCTCCACGGGCCAGGCCCGAGGACCGGGCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA
CTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTCCACCACCTTTCAGGCGC
CGCTCGGCCCCCTCGCCGACCACCCCTCCGGCGGGCGGAACGCACTTCGACCACCTCTCAGGCGCCGACCAGACCCG
CGCCGACCACCCCTTTGACGACCACTGGCCCGGCGCCGACCACCCCTGTAGCGACACCCGTACCGGCGCCACGA
CTCCCCGGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCACCCACCTGCCACCGAGG
CCCCCTCTTCGCTCCTCCAGAGTATGTATGTAACGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGCTTTTACC
TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT
AAGCAACAGAGGGTGAAGTGAAGTTATTTTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCA
TACTGGTTTAAACAAAGGAGGATGAGGTCATAGATTTACAAAATATTTATATACTTTTATCTCTTACTTTAT
ATGTTATATTTAATGTGAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA
TTTTTCTCTGGGATAATTTCTGTAAATTTATGGAAGGAAAAATATTGAAGAATAAATCTGCTTTCTGGAAGGGCT
TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATAACATTGGAGTTTGAGGAAAT
TTGTTGTTTGGTTTATTTTCTCTCTAATCAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGAGACCAAAA
GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGAATAATGTACTGT
TATCTAAGCATTTGCCTTGACTGCACTGAAAGTAATTATTTCTTTGACCTTATGTGAGGCACTTGGCTTTTTGTG
GACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAACC
TGGGTATAACCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTGGGCAAGTAATTTCTTTCACTGAGCTTGT
TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAAT
CTGGTTTGTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG
ACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT
TGTATCATATTGTAGTTTATTTAAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTT
GGGAGGCCAAGGCGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCT
CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
AGAGGGAGACTCTGTCTTAAAAA

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FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRS LPS L GGLALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATAPTAQA PRTGPPRA
TVHRPLAATSPAQSPET TPLWATAGPSSTTFQAPLGPSPTTPPAERTSTTSQAPTRPAPTTLSTTTGPAPTTPV
ATTVPAPTTPRTPTPDLPSSSNSSVLPTPPATEAPSSPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLN YTSGLCQPCDCSPHGALSIPCN R
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 285

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGACATGCTGCTGCTGCTGCTGCCCCCTGCTCTGGGGG
AGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTTCGGTGACGGTGACAGGAAGGCCTGTGT
GTCCATGTGCCCTGCTCCTTCTCTACCCCTCGCATGGCTGGATTTACCCTGGCCCAGTAGTTTCATGGCTACTGG
TTCCGGGAAGGGGCCAATAACAGACCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAG
ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCTGAGCATCAGAGATGCCAGAAGA
AGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT
GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCAGAAT
CTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCC
CCCCGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTC
ACCTGTGACGTTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTACCCGCT
CAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCAGAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA
CTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCACTTGATGCACTTGACAGCAATCCCCCTGCCAGGCTGAGC
CTGAGCTGGAGAGGCCTGACCCTGTGCCCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC
CTGCAGAGCAAAGCCACATCAGGAGTGACTCAGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTTGGTCTTCTCTG
TCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGGCGTGGGAGAT
ACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTCAGCCTCTCAGGGGGCCCTGACTGAACCTTGGGCAGAAGAC
AGTCCCCCAGACCAGCCTCCCCAGCTTCTGCCCCCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATC
CACAGATGAGAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCAGAGGC
TGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAGGC
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAG
ACAGACAAATTCCTA

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FIGURE 286

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNI
PGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPLDPSTTRSSVLTLPQPQDHGTSLTQVTFPGASVTTN
KTVHLNVSYPPQNLMTVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWWHLRDAAEFTCRAQNPLGSQQVYLNVSLSQKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDTGIEDANAVRGSASQGPLTEPWAEDSPPDQPPASARSSVGEDELQYASLSFQMVKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

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FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGGCGGGACTGTCTGTCTGGGGGAGCCGCCCAGGAGGCTCCTCAG
GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCGGCGGGCCCAATGCCACCCTCATTCTGGCC
ATCGGCGCTTTACCCCTCCTCCTCTTCAGTCTGCTAGTGTACCAACCCACCTGCAAGGTCCAGGAGCAGCCACCG
GCGATCCCCGAGGCCCTGGCCTGGCCCACTCCACCACCCGCCCAGCCCCGGCCCCGTGCCATGCCAACACCTCT
ATGGTCACCCACCCGGACTTCGCCACGCAGCCGCAGCACGTTCAGAACTTCCTCCTGTACAGACACTGCCGCCAC
TTTCCCCCTGCTGCAGGACGTGCCCCCTCTAAGTGCGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCCTCC
CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
CGCCTCCTCTTCCTGGTGGGCACAGCTCCAACCCGCACGAGGCCGCAAGGTCAACGGCTGCTGGAGCTGGAG
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTTG
TTCTTACAGTGGCAGGAGACAAGGTGCGCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
ACAGACAACATGGTCTTTCTACCTGCAGGACCATGACCTGGCCGCCACCTCTTCGTGGGGCACTGATCCAAAAC
GTGGGCCCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGACTCAGAATGAGCGGTACCCACCC
TATTGTGGGGGTGGTGGCTTCTTGCTGTCCCGCTTCACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGGAC
ATCTTCCCCATTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCCACAGCGGC
ATCCGCACGTCTGGCGTGCGGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG
CTGGTGCACCGCTTCCTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACCAGCCCCAACCTCACCTGCGGC
AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGGCGAC
ACCTTCCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAGGTTTGATGA
GTGAATATTTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
GGCTGGAGGAATCCAGAAAATATCCATCTTCTTTTTGTGGCTGCTAATGGCAGAAGTGCTGTGCTAGAGTTCC
AACTGTGGATGCATCCGTCCCGTTTGTAGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCAGACAGGGATGCTA
AGCAGTGCACCTGCAGTGGTTTAAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAAACTCCTGTGTC
CACATAGAGCTGACGTGAGAAATATCTTTCAGCCCAGGAGAGAGGGGTCTGATCTTAACCTTTCTGGGTCTC
AGACAACTCAGAAGGTTGGGGGATACCAGAGAGGTGGTGAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
ATGCTGTAATGCTGGAGGTGTGGGCAGAGGAGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
GGGTCTCATTAGGAGCCCCCATCCCTGTGTTCCCCAAGAATTAGAGAACAGCACTGGGGCTGGAATGATCTTT
AATGGGCCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTAGGTCTCCAGCAGCCT
CCCTCACCCAGTATGTTTTACAGATTACGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCAGCTTCAGG
CCTCAGTGTCTGCCAGTCAAGCTTCACAGGCATTGTGATGGGGCAGCCTTGGGAATATAAAATTTTGTGAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRRRRPNATLILAIGAFLLLLFSLLVSPPTCKVQEQPPAIPALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRHFPLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGRERKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTGDIQWDFHDSFFNLTKQVLFLOWQETRCANASFVLNGDDVFAHTDNMVFYLO
DHDPGRHLFVGQLIQNVGPIRAFWISKYYVPEVVTQNERYPYCGGGFLLSRFTAAALRRAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPCFYRDLLLVRHFLPYEMLLMWDALNQPNLTCGNQTQIY

Important features:**Type II transmembrane domain:**

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

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FIGURE 289A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCATGGGCCCCCGGGTGGGCAGGGGTGCGCGCCGCGCTGCGCGCCCGCTGGCGCTGGCCTTGGCGCTGGC
GAGCGTCTGAGTGGGCCTCCAGCCGTGCGCTGCCACCAAGTGACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCCTCCGCGCGGTTCCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAGACAACCAGGTCAG
CGTCATCGAGAGAGGCGCCTTCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT
CCTTCAGAAATTGCTTTTCCAGAGCAGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCCAGGGGAT
CCCGAGGAAGGCGTTCCGCGGCATCACCAGATGTGAAGAACCCTGCAACTGGACAACAACCACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT
GAGGGGCTTCAACGTGGCGGATGTGCAAGAAGGAGTACGTGTGCCAGCCCCCACTCGGAGCCCCCATCCTG
CAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACGTGCGACAATAACATCGTGGACTGTGAGGAAAGGGCTT
GATGGAGATTCTGCCAACTTGCCGGAGGGCATCGTCGAATACGCTAGAACAAGAACTCCATCAAAGCCATCCC
TGCAGGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCCTTCCAGGGCCTGAAATCACTCACATCGTGGTCTGTATGGGAACAAGATCACCAGAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACTCAACTTGCTCCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCCCTGTCAGTCCATCCAGACACTCCACTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCGCGACTCGCCAAACA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCGTGTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTTCCAGCAGCA
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCT
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTCAACGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTTCATGGAGCAGCCAGCGTGCAGGAGCTGATGTGACAGGGAACAGCTGGAGACCGTGCACGG
GCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACTTGATCAGCTGTGTGAGTAATGA
CACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGGTTGAGGAAGAGGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCTCAAGGA
GATTCCTATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACACCTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACAT
GTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCCTGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCGGTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCCTCTCCAG
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCC

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FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTGAGCATGGAGGCACC
TGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
ATCAACCCAGATGACTGTGAGGACAACGACTGCCAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
TGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC
TGTGAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGGAG
CTCTGTGAGACAGACAATGATGACTGTGTGGCCACAAGTGCCGCCACGGGGCCCAGTGGTGGACACAATCAAT
GGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCCCTTCTGTGAACACCCCCCACCCTGGTCTACTGCAG
ACCAGCCCATGCGACCAAGTACGAGTGCCAGAACGGGGCCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGC
TGCCACCAGGCTTCGCCGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
GAACTGGCCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC
CTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG
ACGCTAAACCAGACCCTGAACCTAGTAGTGGACAAAGGAACCTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA
GCAGTGGGCATCAACAGCCCCCTCTACCTTGGAGGATCCCCACCTCCACCGCCTCTCCGCCTTGCGCCAGGGC
ACGGACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
GCCCTCCCACCACAGTCCCTGGGGGTGTCACCAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCCACTCTGCGACCAAGGAGGCCCGG
GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCAT
GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
GCCTCCAAGGTGCCCATCATGGAATGTCTGGGGGCTGTGGGCCCCAGTGTGCCAGCCCACCCGACAGCAAGCGG
CGGAAATACGTCTTCCAGTGCACGGACGGCTCCTCGTTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGGGCTGC
CTCGCGTGTTCCTAAGCCCCCTGCCCGCCTGCCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
GTGGGACCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA
TATTGTAAATAAACAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 290

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNLQVLPPELLFQSTPKLTRLDLSENQIQGIPR
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEILTLNNNNISRLVTSFNHMPKIRTLRLHSNHLCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGAFTQYKKLKRIDISKQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTIKGLFAPLQSIQTLHLAQNPFCVDCCHLKWLD
YLQDNFIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLV
IPSHLPEYVTDLRNDNEVSVLEATGIFKKLPNLKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLKRKRIVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNEESSQLSPRCPEQCTCMETVVRC SNKGLRALPRGM
PKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLILSYNRLRCIPVHAENGLRSL
RVLTLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTPT
HREQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGDCTVPINTCIGNPCQHGGTCHLSDS
HKDGFSCSPLGFEGQRCIEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLCQHEAK
CIPLDKGFSCCECVPGYSGKLCETDNDDCAHKKRHAQCVDTINGYTCTCPQGFSGPFCEHPPPMVLLQTSPCDQ
YECQNGAQCIIVVQQEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHVELVTNLNQLNLVVDKGTPKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS
DQGEFPYCLCPGFSGEHCQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFQ
CTDGSSFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

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FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAAACTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAACTATTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCT
CCCAATATTCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTTAAGAAAATAAATATTTCCATTTAAATGTC

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FIGURE 292

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

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FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCAATAAGTCCCCATGCAGCACTGGAGAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAACAGCATCTTATTACTCACCCTATGGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTT
AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAACCTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTT
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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FIGURE 294

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVIIPVVYDFGDAQKTASYISP
YGQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSSS
REITEAAVLLFYR

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FIGURE 295

CAGGCCATTTCATCCCACTGTCCTTGTGTTCCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGTCATGTGTTAAAAA
CGCCAAGCTGAATATATATCATGCCCCCTATTAAAACCTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG
CTTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT
CACTTCCCAGATCTGCTTCTCACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGCTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGCCCAAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCACTTCTCAGAAGCAATAGAAAAGTTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACC
AAACTGCTGGTATTAATCAGATTGTTTTTAAGATCTCCATTAATGTCAATTTTTATGGATTGTAGACCCAGTTTTGA
AACCAGAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCTATATACACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTAAAGTTACAAATGTGGTGTCAATCCATGTTGAGCAGAGTATTTTAATTATATTTCTCGGGATTAT
TGCTCTTCTGTCTATAAATTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCGAAGTGT
TCACTGTCTATCTGTTAGGGAATTTTGTGTTGTCCTGTCTTTGCCTGGATCCATAGCGAGAGTGTCTGTATTTTT
TTTAAGATAATTTGTATTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAA

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FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRLLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMOCPIAVNSGGPLESIDHSVTGFLCEPDVHFSEAIEKFIREPSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTCLLV

Signal peptide:

amino acids 1-15

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FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATTCAGGGATTACT
CCAACGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTG
CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA
TCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG
AGTAACCTTTGCCCTCCTCTAAAGCTTTTCAAGAAGTATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTACACAGATGGTAATGGGTAGTACATTTGAA
GATGATCAGGAAGTCATTTCGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
GGGTCACCTTGATAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG
AACATCATAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT
AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAAATTGTGTACC
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGA
AATGGTCCTGTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCGAACT
GCCAACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATTCCTAGAGAG
ACCCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
GATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCTCCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
TTGAGGTTTGCATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
TATTAAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAAAATCTATGTTG
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

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FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVSLGTVDLVKQHINPNKTSDFETMLKSLLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLLKLSEELL
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYE
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
NTWPSPHKFDPRFDELVMKTFSSLGFGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 299

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA
TGACAAGCAGGACATTTCAGCTGGTGGCCGCGCTCTCTGTACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCTTCTGCAGTGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTCGTCACCGTCTTTGGGCTGAAAAGAAACCCCTTCTGATTACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCCTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAA

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FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVTEMALEFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 301

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGTGCTGC
TTCGTGTTCTGCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCAGATTACAACTACCATAGTGATACCCCCTACTACCCATCTGGGTGACCCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGTTCTTGCCATCCTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTG
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTCAGACCGGGGTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGAGAGCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

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FIGURE 302

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF
YSTDYRLVQKPCPDYNYHSDTPYYPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

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FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGTATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 304

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLPGTVGIHG
DSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSCLKCLLCQDKNFLLYNQSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 305

[illegible]

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FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGGLNVQQQLHPHVLPFVFTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVDGSLPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 307

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAAATTTTTTG
GGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAACA
ACTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCTTCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAGTC
TGCAGGCATTTAAATCCTTCTGAGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTT
TAGACAAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGGCTT
ACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGACCTGGCGAGGAGGGTGA
AGATTGGACATTTCGTTTTGAAAACCGGCCGATGTATGTACTGAAGTTCAGCACTGGGAAAGGCGTGAGGCGGCCGG
CCGTTTTGGCTGAATGCAGGCATCCATTCCCAGAGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGA
TTGTATCTGATTACCAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTCCTGTGG
CCAATCCTGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATCCTGGAA
GCTCCTGCATTGGTGTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAGGGAGCCAGCGACAACCCCTT
GCTCCGAAAGTGTACCATGGACCCACGCCAATTGGAAGTGGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA
AAAAGGGCCCAGATGCCGAGGAACTCGACAAGGTGGCGAGGCTTGGGCCAAAGCTCTGGCTTCTGTGTCGGGCA
CTGAGTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA
ACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACGGGGACCTATGGCTTCCTCCTGCCAGCTAACCAGA
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTT
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG
TCGTGTGCTCCTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTGCTGTTTTTGATG
AGCCTTTTGTCTGTTTCTCCTTCCACCCTGCTGGCTGGGCGGCTGCACTCAGCATCACCCCTTCTCTGGGTGGCAT
GTCTCTCTCTACCTCATTTTTTAGAACCAAGAACATCTGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGC
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCACCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTT
CCTTTAATTTCTCGCAGTCTTCTCTGGAAAATATTTTCTTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAGGT
CTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTTGCTCTTGTGTCAGGCTGGAGTGTGA
TGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTCAAGCAATTCTCCTGCCTCAGCCTCTTGAGTAGC
TTGGTTTTATAGGCGCATGCCACCATGCCTGGCTAATTTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGT
CAGGCTGGTCTCAAACCTCCAACCTCAGGTGATCTGCCCTCCTTGGCTCCCAGAGTGTGGGATTACAGGTGTG
AGCCACTGTGCCGGGCCCCCTCCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCACTGTGC
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCAGTGTGACCAGGATGGCGGGAGGG
GATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGCAGGATGGTGAAATT
ATCCCCATCTGTCTAATGGGCTTACCTCCTCTTGGCCTTTTGAACCTCACTTCAAAGATCTAGGCCTCATCTTAC
AGGTCTTAAATCACTCATCTGGCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCT
GTGTTTCTTGTCTGTTTGT
TTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCTCTGTTTTCATTTACCT
CAGCACGTACCATCTGTCCCTTTGTTGTTGTTGTTTGTGTTTTGCTTTTACCAAACATGTCTGTAAA
TCTTAACCTCCTGCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAA
AAAAAAAAA

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FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYHSLEAIYHEMDNIAADFPDLARRVKIG
HSFENREMYVLKFSTGKGVRRPAVWLNAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP
DGYVYTQTQNRLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDFTQKHGN
FKGFIDLHSYSQLLMPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTYGFLLPANQIIPAEETWLGLKTIMEHVRDNL

Signal peptide:
amino acids 1-16

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FIGURE 309

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCCTAAGGAACCCAGGCATCCAGCTGCCCCAGCGCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACCTTCAAGTCCC
CTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTCACCAACTCTGAGTTCATACAACTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACCTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC
CAATTCTGAGTCCAGCACACCCTCCAGTGGGGCCAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACCTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTAGGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCCCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCAACACAGCCACCAACTCTGGGTCCAG
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACCTCCCATAGTGCATCTACTGCAGT
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAAGTGGTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGACCTGGGCACCAAGACCTGGTTTCTCTTT
CATTTCATCCCAGGAGACCCCTCCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTCACCTTTCT
TGCCTTTACCAGACACTGGAAAGAGAATACTATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC
CTCCATGCTGGACTCCATCTGGCATTCAAAATCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 310

MMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVSSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTTSNGA
GTATNSESSTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSSGASTA
TNSDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGANTATNS
ESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFWRRPVSSIAMEMSGRNSGP

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 510-532

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FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGCGCGGCTACGAAGAGGACGGGGACAGGGCGCCGTGCGAACC GA
GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCGCGGTCTGTCGCGGT CG
TGCCGGGCCCCGCTCCCCGCGCGAGCGGGAGGAGCGCGCCACCTCGCGCCCGAGCCGCGCTAGCGCGCGC
CGGGCATGGTCCCCTCTTAAAGGCGCAGGCCGCGGGCGGGGGCGGGTGTGCGGAACAAAGCGCCGCGCGGGG
CCTGCGGGCGGCTCGGGGGCCGCGATGGGCGCGGGCGGGCCGCGGGCGGCGGGCGCTGCCGGGCGGGGCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGGGCGGGCGGC
GGCGGCGGGCGGGCCCCGGCGGGCGGAGCGGGCGGGCATGGCGCGCGCGGGCGGGCGCGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCCCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGCTTCGAGCTGAAGCGAGCGG
GCCCAGGGCGCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGCAGGGCGGGCGGCTTCCAGGCCGGCGGGCGCGCG
GCGATGCGCGCGGGGCGCAGCTCTGGCCGCGCGGCTCGGACCCAGATGGCGGGCCGCGCGCAGGAACCTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
TTCCTGGGAAAGTTCACTTCTCTCAAGTGAGGGTCTGACACATCTGTACCAATCCAGTAGTGCCACTACGGG
GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTCAATGATGCTCAAGTACATGCACGACCCTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
TGAACAGCAGCGAGCCCCCTCTTCTTGGGCGAGACAGGCTGGGCACCACGGAAGAAATGGGAAACTGGCCCTGG
AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCCG
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCATGAGGACGTGGAGGTGGGAAGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGT
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACCCCCAACAAAAACCCACCCTACCAGT
ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
TTGTCTGTATGAGCAAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
TGAGTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAATACTTGTATTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCGCAGAGGGAAGCCTTGGACGACATTGTATGCAGCTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
TGGATGCACAAAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTCTCAAATCCCTGAAGA
AGCTCGTCCCTTTAGCTCCCTGGGTGAGGATGAGCACAAGAACCCAAAGATAAAAAAGATAAACATACTGA
TTCCTTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATTCTGACTCCAACCTGACAAGGCCAACAAAGTTGAACCTGATGA
GAGATTACCGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
CCCTGGAGTAGGATCCTCCAGTTTAAACAATGAATCTTGGCTCTTCTTCTGCGACGTCGACCTCGTGTTTACTA
CAGAATTCCTTCAGCGATGTCGAGCAAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAAGTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTGTCCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTTCAAAAATTTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTCTTACATAGGACTCCTTAAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAACCTTT
TTTAAAAAATGTTTTCTTTTGAGACCTTTTGCTCCAGTCTATGGCAGAAAACGTGAACATTCCTGCAAGTAT
TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTGTTAACATTCCACAGATTCTACCTTTGT
GTTTTGTTTTTTTTTTTACAATGTTTTTAAAGCCATTTTATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTTGCTTTCAGGAGAGCTTTCAGAGTTGATCATTTTCTCTCATGGTACTCTGCTCAGCATGGC
CAGTAGGTTTTTTGTTTTGTTTTGTTTTGTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATTTCCCTGCCTTTGCCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTGTATTTTTAGTAGAGACGGGTTTTACCAT
GCAAGCCCAGCTGGCCACGTAGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTCTCG
TGGTAGTTTCATTCCGCCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTTTCTCTTCTTACCCCT
CTCTTTAAAGGCTAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGATACACAGACT
GAAACATACACATACACCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTTCATCTGTCTGT
TGTTATGTGGGTGGAGATGGTTTTTATTCTTTTATTACTGTTTTGTTTTATCTTTGTATCTGAAATACCTTTAA

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FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTCCCCTCC
TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTGTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAA

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FIGURE 312

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTIPGKVQFFSSEGS
TSVPPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDVYIKGDRLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALFGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTHE
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQRQREEILEW
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGDIVRVGGFDVSIQGWGLEVDVLEFNKVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
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Signal peptide:
amino acids 1-23

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FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTGACA
GGTGGGAGGCTGGAAGTATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTCATGGAAAGGGATTTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTTCATGCTGAGTCCCTTTTTACCTTTGATGTTTGTAAACCCATCTTGGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCCACCTGCTGGCATTATTGGAGACCA
TGTTTGGTGTAAGGTGATTATAACTGGGGATGCATTTGTTCCCTGGAGAAAGAAAGTGTCATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAATTTGCCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTGGTTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTACGAACCACTTCAACTCCTCATATCCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTCACGTCCACCGGT
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGCG
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTTATTTTACCGGAC
AGAGTGTCATTCCACCTTGCAAGTCTGAAGTCAAGGTCCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAAGTTCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTTCATGACTATGTGGAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCACTTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAACTCTCTGAA
TGTAATTTGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

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FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSGIMVSWKGIYFILTLFWGSFFGSIFML
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF
CDIHEPLQLLI FPEGTDLTENSKSRSNFAEKNGLOKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHL LQGDFPREIH FHVHRYPIDTLPTS KEDLQLWCHKRWEEKERL
RSFYQGEKNFYFTGQSVIPPCKSELRVLVVKLLSILYWTLESPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIELACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

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FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
CCTCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTTCATAGTGTGAGATCAACCCACAGG
AATATCCATGGCTTTTTGTGCTCATTTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCAGTTCTTTCAGGAATCAGTTCCA
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCCCAGATTTACGATGAGGA
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATA
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTTCCCCCAGCCCACAGCCAA
GTGGAAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG
CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
GCCCTCACCTTGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT
TGTGATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCT
GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTTCTGATCTGAAAACGTAAACCCATAGAAA
AGTCCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
GGTTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
GGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
GTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTACATTCAATCCCCATTTTATCAG
CCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCTTGGACTATGAGGGTGGGACCAT
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCAT
ATGTCCAGTGTCTTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAGCCTGCGC
ACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
GCAGCGGCAGTCACAGCTTCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAACCTCCATC
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGGACAGT
GATTCCTGCCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAAGTTTGA
GGGCACAGTGTGCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCATATAAGCCAG
CATTACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACCTACAGGTCCA
TATCCCTCATTAACACAGACACAAAATTCTAAATAAAATTTTAACAAATTAACTAAACAAT
ATATTTAAAGATGATATATAACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAA
TATTTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA
AAAAA

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FIGURE 316

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDGRGKNNVTLSFNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

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FIGURE 317

GCACCTGCGACCACCGTGAGCAGTCATCGCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGCTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTTGGGATTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAATTGAAAATCTAATATGGCGATAAAAATCATTGT
CTACATTAAAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTTCAGTTTCACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGGTTCTTAATCCAGTGAGTGATAACAATTCAATGCACTCCCCTGCCA

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FIGURE 318

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQTP
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRIILIILHQ

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FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGTGGGAACCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT
GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTA
CTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGACAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTGAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTTAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA
GCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATAACAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTGACTTGTTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTCAGCAAATATCCA
TTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACTAA
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACACTACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG
TACTTGTTCTAAGCAAATTAAAGCAAATATTTAATTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

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FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTNAVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSQNHRLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

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FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCCGCAAGGCGGCA
TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCTGGTGATCCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT
GGACTTCCGGGGCCTCCCTGGGAACCTACCACAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA
CAACACCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCTAGAAAGAGGGGACCGAGAGCTCCTCCCACTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

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FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIIKLPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGT HKDVLEEGTESSSHSRLSPRKTHLLYILRPSR
QL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

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FIGURE 323

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCC
CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
TCCCTTACGGGGCTCACAATGCGCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC
GCCCCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGATGAGG
GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
ACTTACTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTCTGCTGTTTCTTATCATTGTGGGG
ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT
TTGCTTGTCAATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATG
GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCT
AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTCAGAGAGAGTTTAAAGTCTGTGGAGTA
GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTGTT
AGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
GGTTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTT
CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAAC
TCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
CACACATCCATGGCAAACAGCTTTAATACACACTTTTGAGATGGAGGAGTTATAAAGAAATG
TCACAGAAGAAAACCAAACTTGTTTTATTGGACTTGTGAATTTTTTGAGTACATACTATGTG
TTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
ACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA
TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT
AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
TTCTGATGCTAAATAAATTATATATCAGAAAACTTTCAATATTGGTGACTACCTAAATGTGAT
TTTTGCTGGTTACTAAAATATTCTTACCACCTTAAAAGAGCAAGCTAACACATTGCTTAAAGCT
GATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTTCAGTCGATTTTCAGTTCT
GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTA
GCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCTGCTGGGCTTATATTACACATATAACTGTTA
TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAAAGTGTGATTCAGAA
AGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTTAAAA
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA
AAATAGTGTTCTTTTTCTCCAGAAAATGCTTGTGAGAATCATTAAAACATGTGACAATTTAG
AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAAATTTT
TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT
TTTGTATTATTTCTCAGAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAG
TAA

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FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

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FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCCAGAAGCCCTGTTTCATGGTTGGGGATATTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCCCTAT
GTCTCTTATCTGCGCTTTTGGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTAATTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTCACGCCATCGCTGCAGCTCTTGTTATTCACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTCATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCATTGAGCCTTGCAAACAACA
ATCTCCAGACACTCCCAAAGATATTTTCAAAGGCCTGGATTCTTTAACAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAATGGCTTGGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTTGCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAAAATGCATTTTCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAAACTCAGCTCTATG
TTATTGTGGCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTGCAAATAAAT
TCATAAAAATCCAGGATATTGAAATTTCTCAAATCCGAAAACCAATGACATTGAAACATTCA
AGATTGAAAACAACCTGGTACTTTGTTGTTGCTGACAGTTCAAAAAGCTGGTTTTACTACCATTTAC
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCACGCGTCCTGTAATTTATCAGTGGAACAAAGCAACACAATTATTCACTAACC
ACTGACATTCCTAACATGGAGGATGTGTACGCGAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCTTGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTTTCAAGGAATTAATGTTTCAGGCACCAAGATCATTCACACATGTG
TCCATTAATAAGCGTAATTTTCTTTTGGCTTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTCATAGTTGACTTAAGCGCATGAGACACCAAATTCCTGTGGCTGCCATCAGAAATTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAAATAAGCGTTTAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTCATGTGTACAGAAACAACCTGCCAAATAAAATGTTTACATTTTCTT
TCATA

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FIGURE 326

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLLEGKKPAKPKCPAVCTCTKDNALCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSLANNLQTLPKDIFKGLDSLTVNVDLRGNSFNCDCCK
LKWLVEWLGHTNATVEDIYCEGPPEYKKRKINSLSKDFDCIITEFAKSQDLFPYQSLSID
TFSYLNDEYVVIAQPFTGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSVMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLEASS
FKGNTQIYKHVIVDLA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

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FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA
AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
CAGAAGGATGCCTCCATTCCCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA
CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAGGCGACGGCATTGTGCAACGCCA
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTG
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG
TCATTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATACCAGCGAGTGCAC
ATGCGCTCCAGGAACGTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGCTGTGAGTG
TGGGGTTGGCCGTGTGCTAAGAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
TAACAATGGTGGCTGCAGCCACTCTTGCCCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
CCGGGGCCTGGTGCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAA
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTGGCTGGAGCTCTTCCTGACCAACAC
CTCCTGCCGAGGAGTGTCACACGGCACCCATGTCAACATCCTCTCTCTCAAGACATGTGG
TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
CTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
ACTGGAATCATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAA
TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCACCCTCAAGCTTCGTGACTCCCTCTACTT
TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAAGCTTGGTGGAGAGCTGCTTTGCCAC
CCCCACCTCCAAGATCGACGAGGTCCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCAGGTCCCTGTCTT
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTTCTGCACTGCCGGGTCTTGTCTGTGGAGT
GTTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGG
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA
GGACTAGTTTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTCAGACTTCACACTGTGAGTTCAG
ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTCAAGTGGGCACAGGTCACAGCACTGCTG
AACAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAAGTGTCCACCCAGAA
AGACACTCACCCCATTTCCCTCATTTCTTTCTACACTTAAATACCTCGTGTATGGTGCATC
AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAG
TTACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAAACAGTAT
ATAATTTT

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FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT
GMAGDAMPFTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYVYVRLTKPSVCFHVYCGHFYDICDEDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDEVEGCHNNNGGCSHSCLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLFLTLNTSCRGVSNGTHVNLFLSLKTCGTV
VDVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKLRLDSLYFGIEPVVHVSGLESLEVESCFAATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVVGKDHKEVFLHCRVLVCGVLD
ERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGPIRIDWED

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

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FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCCTCATCAAGGTGATTC
TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA
CAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCC
TGGTCTCCCTGCACTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG
AGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTACAGTACGACAAACAGCACGTCT
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGG
CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC
TCATGAAGCTGCAGTTCCTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT
GCAATGCAGACGATGCGTACCAGGGGGAAGTACCGAGAAGATGATGTGTGCAGGCATCCCCG
AAGGGGTGTGGACACCTGCCAGGTTGACAGTGGTGGGCCCTGATGTACCAATCTGACCAGT
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCAGGAGTAT
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCT
GCTGCCCCCTTTCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT
GGAGCAGCAAAGGGCCTCAATTCTGTAAAGAGACCTCGCAGCCCAGAGGCGCCCAGAGGAAG
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC
AGGCTGTCTTGTAAGGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA
GCCCTGTCCGTCTTACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTTCATTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

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FIGURE 330

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAEACRQMGYSRAVEIGPDQDLVDVEITENSQELMRNSSGPCLSGSLVSLHCL
ACGKSLKTPRVVGGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTG
QGDSSGGLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

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FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTTCGAAATCA
ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAÄCTTCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCTCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAACCT
TCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGT
ACAAGGGGGGCCATGGGCATGCCTGGTGGCCCTGGCCCGCCGGGACCACCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGGCCACCGGGAG
TCAAGGGAGAGGCGGGCTCCAAGGACCCAGGGTGTCTCAGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGG
AAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTTCATGGGGCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTGAGGATTGTTCGGCAGTAGTA
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGTCTGACCCCGAAACCCTTTCACCTCTCTGCTCCCAGGTTCTCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTCCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

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FIGURE 332

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKDDL
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPAGKGDQGPGLQGVPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTLQGGQGRKGESGVPPGAVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYS
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV
```

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 333

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT
CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCTGGC
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTCAGCGAGCCTAGAGAGGGGCAGACTA
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG
GGCACTTGTGGGTTCAGAGCCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGCTACCAGGT
CCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
CAGGAGGGGTCAGAGCCCGTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGAGCCTGGCCGA
GCTGCTGCAGGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATTT
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGCACCAGTGGGGCC
ATCTACTTCGACCAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGCTCTGGCTCCTTC
GTAGCCCCTGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGGTGTACAACCGCCAA
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCATCTCAGCCTTTGCCAATGATCCT
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG
TCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
CTCATCTTCCCTCTCT**TG**AGGACCCAAAGTCTTTCAAGCACAAGAAATCCAGCCCTGACAACTTT
CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC
CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAAGTTTAAGAGAAGAGTAGAGCTGTGGC
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACCCTCCAGCCACCTGCTGCATC
TGTTCTTGCTGCTGCTCCTCCGGTTCCCCACCCAGCTTCCTGCTCAATGCTGATCAGGGACAGG
TGGCGCAGGTGAGCCTGACAGGCCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGGAAGGGTGGGAAGGGCCTGGA
GTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCCTTCTATGCTGGATCCCAGAT
GGACTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAAGTGTGTTTGCTCTGGCTGAGAGCA
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
TCTTGCTTGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC
TCTGACTGCTGCCTCCTTCTCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
CATATCCCCTATCTCTCTTCTCCTGATCTGTGCTGTCTTATTCTCCTCCTTAGGCTTCCT
ATTACCTGGGATTCCATGATTCACTCCTTCAGACCCTCTCCTGCCAGTATGCTAAACCCTCCC
TCTCTCTTTCTTATCCCGCTGTCCCATTTGGCCCAGCCTGGATGAATCTATCAATAAAACAAC
AGAGAATGGTGGTCACTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGG
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAATAAATATCAAACCTGTATACTAA
AATTAAAAA

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FIGURE 334

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGFLIFPL
```

Signal peptide:
amino acids 1-32

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FIGURE 335

[illegible]

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FIGURE 336

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFIH
GRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

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FIGURE 337

GGGCGGCGGGATGGGGGCGGGGGCGGGGCGCGCGACTCGCTGAGGCCCGACGCAGGGCCGGGCGGGGCCA
GGGCGGAGGAGCGCGGCGGCCAGAGCGGGGCGCGGAGGCGACGCCGGGACGCCCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCTACTGGCTCTGCTGACCTTGTGCCCTTGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCGCTGCTGGCCTTCTGAAGACCCA
GTTCTGTCTGCACCTGCTGGTGGCTTGTCTTCTGTGGTGGTGGTCTGGTCTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGCTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACGGACAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGACCGGGACACCGTGGTCCAAGGGCTGAG
GCGCTTGTGGACTACCCGAGTACATGTGGTTTCTCCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA
CCGCTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCAACCACGCGAGTCAAGTGCCTCCGGGGGACAGTCGCAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
CAAGAACCCGTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGGAGGCCGTGGACCTCCTGAA
CTTCTGTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTTGTCTTGGCGCTCTTTGCCAGCGGATCACC
TCTCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAACAAAAAACCCAGAAATTTCTGGAGTTGAACGTGTGTAGTTACTGACATGAAAA
ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCAGAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCAT
AATCAAAGTGTCAATGACAAAGAATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG
ATCAGATTAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCTGACCTCTTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCCCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTTAAGGCTGAATGATGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCACCATGCTGGCTAATTTTGTATTTTGTAGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGGAATGTCTGTTCAAGTCCTTTG
CCTTTTTAAATTTTATTATTTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTGTATTTTGTATTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTCAACCATGA
TGCCAGGCTGGTCTTGAACCTCCTGAGCTCAAGTGTCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACTCCAAAAATCAACACACACACAAAAAACCATCTGATTCAAATGGGCA
GAGGGGCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

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FIGURE 338

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVVSGLVINQVQLCTLALWPVSKQLYRRLNCRSLAYSLSQSLVM
LLEWWSCTECTLFQDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGGKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTF LGFVGAASFGVRRLLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

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FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTGTTCCCT**TAA**TGTGGTATGCCATGGGGTCTTTCACAAAGCCTTTCCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGATGCTGGTCCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGGAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAA

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FIGURE 340

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHS LQCPGAATRH IHL CVCF SFALALGH FLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRRE
GKINFYTN GDSWGLR PASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

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FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTCGCGGCGGCGGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCGGACGTCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTCGTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 342

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDQPSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTQ
```

Important features of the protein:**Transmembrane domain:**

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

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FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTTCATAGGCG
ATGGCTCCCCTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTT
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACCTG
TGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTCCGCCCGCATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTGGCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAATAAAAAAGAATTATGGTTATTT
GTAA

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FIGURE 344

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD .
```

Signal peptide:
amino acids 1-15

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FIGURE 345

[illegible]

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FIGURE 346

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61; NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKS AKKPQSSSTEPARKPGQKEKRVRP EEEKQQ
AKPVKVERTRK RSEGF SMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVM EKA AEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEK LAGEELAGEEAPQEKAEDKPSTDL SAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLD RPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

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FIGURE 347

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTATCATATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCAGCTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCCTTTTTGGGTTCATC
AGAAGGACTGGATTTCAAACCTCTTCTCTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAAGTGGAGCATTTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCTACTCATGACCACCACCTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
AGGAGGACAACGCAGCCTGATAAAACAAGTGGACGACTTTTCTTAAAGGCCAGACTGATTTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGGAACAGACATTGGAAGTGTCTTCAAAGTTGTCAGCATTTCAAAGGAAAAGTGAATATGGA
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCCTGGGATGGAAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCAGTGCTGGGACATCGAAGACAG
CATTAGTCATGAAAGTGTGATGAAAAGTGTATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAACGGAATATGGGCTACTGATTGCAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAGA
CTACATCCAAATCCTTAGCAGGCCAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGTCCCTAGAGCTGTAGCCACCTAGTTTTCTACTTAATTTAAAGAAAAGAAATCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACAGTTTT
CCAAGAACAATCTTGCACAAGCAAAGTATAAGAATTATCCTAATAAATAGGGGTTTACAGTTGTAAATGTTTTA
TGTTTTGAGTTTTGGAATTTATTGTCTATGTAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACCTCCCATATC
AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGCCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTTCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTCCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACATCACAAATAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAACATAAATCTTCTGAAGAAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTTCACTATATATTTTCTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTACTGC
CTTTATTCTCTCCTGTATATTGGATTTTGTGATTATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAA
AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTTGAATTTAACAATAAATAAGCCTGCTACATGT

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FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTyKDLLLSNSCIPFLG
SSEGLDFQTLTLLDEERGRLLLGAkdHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFPDQQ
PFASVMTDEYLysGTASDFLGKDTAFTSLGPTHdHHYIRTDISEHYWLNgaKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIpGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSaVcVYSMADIRaVFNgPYAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFK
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVVLEELQIFKHSS
IILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYgKACADCClARDPYCAWDGNACsRYAPTsk
RRARRQDVKYGDPITQCWDIEDSIShETaDEKVIFGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYyCKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKGgPKWKHMqEM
KKKRNRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

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FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCCGCGGGGAGCAGA
CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
CTCAGCAGTTTTCAGCCAGCAGGGACTGATCAGGTGTGTCTCTGGAGTGGGAGCAGAAGGCGTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTTCAGCGCTTGACCAGCCGAGCTGCCCGTGAATAAGATCCAGAACCATGGGCATC
GGGTGAGGTGGGGGGGCACAGGTGTCTGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTGAGGGTGTCTGAGCTACAGAGGGGAGGGAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
GAGCAGTGTGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTTAGTTCTGTAGCCCCAGGT
AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCATCACTAAAGTAGGGCCAATAATAGACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCCGGGCACAGGTGAGCC
AGGTGAAGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
TGACCCAGGGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC
CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
AGCTGACAAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCAATCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCGGGCCCAAGATGGAGTAGATGACG
GCTTCTGGAGGGGAGAATTTGGGGGCCGTGTTGGGGTCTTCCCTCCCTGCTGGTGAAGAGCTGCTTGGCCCCC
CAGGGCCACCTGAACCTCTCTGACCTGAACAGATGCTGCCGTCCCCTTCTCTCCAGCTTCTCCCCACCTGCAC
CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCTCTGG
ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACTCCCCGCGGCTAAAGCCCCGATCCTGGCCACC
CAGATCCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCACTGATGCTGTCTCTTCAAGCTGTGAGCAG
CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCCCTCACCTCCAAGGGT
GGAAACTTGCCCCCTTCCCATTTCTAGAGCTGGAACCACTCCTTTTTTTTCCATTGTTCTATCATCTCTAGGACC
GGAATACTACCTTCTCTTCTGTCTATGACCTATCTAGGGTGGTGAATGCCTGAAATCTCTGGGGCTGGAAACC
ATCCATCAAGGTCTCTAGTAGTCTGAGCCACCTCTTTCCCACTGGCTCCATGACCCACCCACTCTGGATG
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCTTGGGAATCAGGAGCTGGAGCCAGGATCGGAAGCAG
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG
CTAAGAGGGCAGGGGGCCTACGGTGTATTGCTTTAGGGGCCACCACGGGCAGGGGCCTGCTCCAGCTGCCAC
GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
AGCTGGGGGCACTGCTGTCCAGTGGAGGGGAGGGCTTTACGCCCCACCCACCCCTGGCCTGCCAGCTGGTAG
TCCATCAGCACAATGAAGGAGACTTGAGAGAAGAGGAAGAATAACACTGTTGCTTCTGTTCAAGCTGTGTCCAGC
TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGATTTATAGCAAAGGCTAAGCCTGC
AGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGGAGGGG
TCAACAATGAGAGACCAGGAGTAGGTCTTATCAGTCCCCCAGAGTAGAGAGCAATAAGAGCCAGCCAGTGC
AGTCCCGCTGTGTTTTCTTACCTGGTGATCAGAAGTGTCTGGTTTGGCTTGGCTGCCATTGCTCTTGGAGTGG
GCAGCCCTGGGCTTGGGCCCCCTCCCTCCGGCCCTCAGTGTGGCTGTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
CACGAGGGGTTAGGCTGCTGTCCCTGAGTCCCTCATCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGGCAGCCTTCCATGGCAGGCATCCCTGCCTTGGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
GGTCTGTCCCCCACCAGAGCCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
TCTCAATGTGTGTACCCGGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
GCCCTCCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCTTCTC
AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCACTT
TGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTTCCCTGGAGCACCTGCCCCACCTGCCCC
CAGAGAACACAGTGGTCTCCCCTGTCCGGGGCGGCTTTTCCCTTCCCTGGAGCGTCCCTCAGGCACAGTGGAG
GCCTCTTGTCTGCGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
CGTCTGACAGGCTGGAGGTGGCATCCACACTGGACAGCAGGAGGAGGGAGTGGGGTAACATTTCCATTTCCT
TCATGTTTTGTTTCTTACGTTCTTTCAGCATGCTCCTTAAACCCCAAGCCCCAATTTCCCCAAGCCCCATTT
TTTCTTGTCTTATCTAATAAACTCAATATTAAG

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FIGURE 350

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPLSLPESSQSDNPGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

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FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCTCAGCCCTTCTGAAAACTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCAGGCTACAGAGAGGAGCTTCCAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCCTGCCTCCTGCTCCCATTTGTGCCGCTCTCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCTCTCTCTGCCCTCAGCCGGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT
CGTGTTCAGAGAAAGCTCAACGGCAGCGTCTGCTGGCTCGGGCGCCCTGCCAGGCTGTGTGCCGCTTGCA
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA
CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGAGCCCTGTTAGGCGTGTACAATATCGGGGGGCTGAACCTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAATCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAGCCCCAGCCCCAGCCCCGAAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCCACGGTGC
GGGGCTAAAGCGTACCTGCTAACAGTATGGCAGCAGCAGCCAAGGCCCTCAAGCACCCAAGCATCCGCAATCC
TGTACGCTTGGTGGTGAATCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGGCCCCAAGTGGGGCCAGTGTCTG
CCAGACCTGCGCAGCTTCTGTGCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTCTGTTTACCCGTCAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGTCA
TGAAGTGGGTGATGTCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC
CTCTCGCCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT
CATCACTGACTTCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCCGGGCCGACTCACGCCATTGTCC
ACAGCTGCCCGCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAACA
CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCGCACAGGCTGCATGGGTGGTGCCTCCACATGGACCA
GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTGAATGCTCTCGGACCTG
TGGGGTGGTGTCCAGTTCTCTCCCGAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCGTACCCGCTTCCGCTCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCCAGGGCCCATGGACTGGGTTCCTCGCTACAC
AGGCGTGGCCCCCAGGACCAAGTGCAACTCACCTGCCAGGCCCCGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCCGTGTCCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCATGCATCCATGCTGG
CTGTGATCGCATCATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTCTGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTCAAGTACGGATACAACAATGTGGTCACTATCCCCCGGGGGGCCACCCA
CATTCTTGTCCGGCAGCAGGGAAACCCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA
CAGCGGGGGCACTGCAGCCTCAGAGACACTGTGAGGCTATGGGCCACTGGCCAGCCTTGACACTGCAAGTCTCT
AGTGGCTGGCAACCCCCAGGACACACGCTCCGATACAGCTTCTTCTGCCCCGGCCGACCCCTTCAACGCCACG
CCCCACTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCCGGCGGCGCCCTGGGCGGGCAG
GAAATCACTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTCTGCTGCCCTGGGAGGCAGTGATGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAACTGCCCCCTCTGCCCTGCGGCTCACAGGAGGAGGGGGAAGGCAGGAGGGGCTGGGCCC
CAGTTGTATTTATTTAGTATTTATTCACTTTTATTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTCTCT
TTCTTGAATTTTATTTTGGGAAAAGAAAGTCAAGGGTAGGGTGGGCTTCCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTCTTTCTTTCTTTCTTTTGTGAGACAAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG
GCACAACTCGGCTCACTGCATCCTCCGCTCCCGGTTCAAGTGAATCTCATGCCTCAGTCTGATGCTAGTCTG
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTTGTTTTGTTTTGTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCCGACCTGGGTTCCAGCAATTTCTCTGCCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCCGCTAATTTTTGTATTTTGTAGTAGAGACGGGTTTCAC
CATGTTGGCCAGGCTGGTCTCGAATCCTGACCTTAGGTGATCCACTCGCCTTCTCTCCAAAGTGTGGGATT
ACAGGCGTGAGCACCGTGCCTGGCCACGCCCAATTTTTGTATTTTGTAGTAGAGACGGGTTTCCAGGTTG
TGGCCAGGCTGCTCTTGAATCCTGACCTCAGGTAATCGACCTGCCTCGGCTCCCAAAGTGTGGATTACAGG

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FIGURE 351B

[illegible]

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FIGURE 352

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLQYRGAEHLQPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTMMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPD SRHCPQLPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRFPVPRNGGKYCEGRTRFR
SCNTEDCPTGSALTFFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGA
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFVPRPTPSTPRPTPDWLH
RAQILEILRRRPWAGRK
```

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

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FIGURE 353

GCGGAAGTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCAATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCTGCG
TCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTTGGTGGCACCCCTGC
TTTGCCTGTCTTCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTCAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAAA
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 354

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQDEA
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 355

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCAGCCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTCAGGCTTCACCGAATGCAGGGCCCTATTTACCATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTCTGTTGGGCTGGGTG
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTGCTACAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTG**TAA**TGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTTAAATATAA
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG
ACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCCAGCTTATCCCCAAG
AAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTTCTAGGAGTTTCCTGAGCTCTCCACTGGAGTCCTTTCTGTGCGGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAAATAA
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCATCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAACTAATTCTTTAA

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FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGWLWRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

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FIGURE 357

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATCGCAACCCATGCCTTAGAAATCGCTGGG
CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTGGATG
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT
GTGAGCTGGGTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA
GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
CCTTCCCATCGCACAACCCAAAAAAGTTATCACACCGGAAAAGAAGTCACCGAGCGTCTACTCC
AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAAATGACA
AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGC
CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTACAGAGAA
TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
TTCAAGCATCTACTCTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA
CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT
AGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTACTATTAATTG
TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATAATGAAGATTAATAATGAAGGCTTTAA
TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA
ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
TTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAAGTCTTTTCCAGGGCTATACTC
AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTAGGAAAGTGAAAATATTTTT
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTT
CTTCTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTGTGTGCGACGTCTGTCTAGCTTAAAT
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

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FIGURE 358

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQ
CKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

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FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFLG

SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDYYQRHYDED

SAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

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FIGURE 361

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAGA
TTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAAGAACCATCAGCCCTC
AGCTGCACCTCCTCCCCTCCAAGGATGACAAAGGCGCTACTCATCTATTTGGTCAGCAGCTTT
CTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCTGGAG
GACTTGAGTGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGGAAAGC
AAGTTCAACATATCAAAGATAAATGAAAATGCGGATGGAAGCTTTGACTATGGCCTCTTCCAG
ATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCACGTAGAC
TGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGATTGTGTCC
GGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTTCAGGCCGGCCACTCTCC
TACTGGCTGACAGGATGCCGCCTGAGATGGAACAGGGTGCGGGTGACCGTGGAGTCATTCCA
AGACTCCTGTCCTCACTCAGGGATTCTTCATTTCTTCTTCCTACTGCCTCCACTTCATGTTAT
TTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAATGGTTTTCTTGG
CTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTATTTGTAAACTGAGG
ACCACAATAAAGAAATCTTTATATTTATCG

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FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGLSDWLCIAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNNLAGIHCAKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

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FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
GGTGAAACTTGGGTCCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
GCAAATGTCAGGACCAGGTTAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGTTGCACCCCTC
CCCACCACACCCCTGCACCAGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
TGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTGAGCCTGGACCCACGTGGCCTCCAGGAGG
CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCCAGGGCCTTCTGAAGG
AGATCATCCTCGTGGACGACCTCAGCCAGGACAACCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCACCTGCGAGT
GCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCACTGGGAACCTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAA
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAATCAGGATTCCCATTCCCCCTCGACCAGGAGGCCACCCTGA
GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC
AAAGGAGACTGGGTTGTGCGACATTCCACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCCATGGTGTGGCTCCTTGCAGTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC
TGTGCTTTGCTGTCAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTCAG
AAGGAAAAGAGAATTTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTACACCTTATTTCAATTGACTGCTGGCTGCTTA

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FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSPVIDVI
DWKTFQYYP SKDLQRGVLDWKLD FHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHYQYQND SHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCEMERLQLQRR LGCRTFWFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQYQLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

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FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCCATGCGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCCTGGTTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCTT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGTACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTGAGCGTTGGTATTTACATTCAATGGAGCTG
AATGTTCAAGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTTCAAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAAATTATTTCCAACA

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FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPA
GVP
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRILIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 367

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTCTGCCTCCTTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

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FIGURE 368

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDGTP
PAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

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FIGURE 369

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGC**ATG**GCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAAGT
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTGAGGGGCGCTGCTCACCGACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCCCCAGAGGCG
CTGGGAGTGTGTCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACGTCACAGACTCGCACGTGCG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC
TGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCACCTGGCTGTCATCGG
GTAGGGCGGGGCCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGTCCCACAGGTCCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACACATAAATAACTGGCACAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG
CACAGGCTGGCTCCCTCAGCTCCACGTCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGGCGGCTGCAGTCCCTTTCTCCCTCAAAGGTCTCCGACCTCAGCTGG
AGGCGGGCATCTTTCCTAAAGGTCCCCATAGGGTCTGGTTCCACCCCATCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA
CATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCCCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCTTCGGACATCCAGGCACGAGGGTGTCGTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSRGDLP

Signal peptide:

amino acids 1-15

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FIGURE 371

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGGCTGCCGCCCTC
TCGGCCACGGCTGGGTGCGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGGCCCCCGACCCCTGAGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTAACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG
AAAAGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGAATTTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTTGTATTCAACTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAAACATGTTTATAAAGTAAAAAA

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FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTROLLSHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLEKNDPLFF
KPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 373

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAACCTGGGGGCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCTGCCCCGTGCCCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCTCCTTGGGGGACTGCTTGGAAAAGTGACGTCAGTGATTCCTGGCCTGAAC
AACATCATTGACATAAAGGTCACCTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCAATCAAGGTCTTAAGCCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

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FIGURE 374

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDQPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHLVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

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FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAAT**ATG**TCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA
TTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTTGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

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FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMVCVNYNDQHPNGWYIWILLLLVLVAA

LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP

APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

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FIGURE 377

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG
ACCCCCGTGTGGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCC**ATG**GCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCGCTCGGGGGGCATCGGCGCGGCC
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGACAGGCTACCCCGGGACTTTGATCCCCTACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGC
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCTCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTCTTG
TGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTTGCACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCCAGTCTTGGCTTCTTGT
CCCCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGGATTTTCATGGTGATCATTAAGAAAAAGAAAAATCGCAACCAAAAAAAAAAAAA

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FIGURE 378

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRC DLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFNVNVLALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

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FIGURE 379

GAGCGGAGTAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGCGGCGACCGTGACGAGAAGCCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGCTTCTTCAGAAATGTTTTTACAATCTC
AAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATTTGGGGATT
GATGTTACTGCACATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTGCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGGAATCTAATTTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGCTTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACTTGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTCAATTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTAATCATTCTGTCAATTTGTTCTC
AATAGATGTAAGTGTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAAATACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAAAAATAGTTGTAAACTCTAATCTTATACCTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTACATACAT
GAATGTTCAATTTAAAAGTTTAAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAATAAGAACATTTAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA
ATTCTAGTATAAAACAAATTATACTTTTATTTAAATTTCCCTTGAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTCATAGTATTTATTTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCAATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

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FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP

VTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

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FIGURE 381

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAAGATTCCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTTTCAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAATGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTATTCTTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAAAATAACCACACATGGCAAAA

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FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQ
PVKGHGTLGESPM PFKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACA
ACCAAATAAATAATGCTGGGATTCCTTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
ACCTATACCACAACAGTTTAGATGAATTTCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCCTATCTGG
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTCCGAG
ACAGCAACTATCTCCGACTGCTTTTCTGTCCCGTAATCACCTTAGCACAAATTCCTGGGGTT
TGCCCAGGACTATAGAAGAACTACGCTTGATGATAATCGCATATCCACTATTTTCATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT
CCCTGACTGCTGCACCAGTAAACCTTCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGCGGCTCATGTGCCAAGCCCCAGAAAAGGTTT
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTCAAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCTATA
TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATA
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
CTGCCATCATTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT
ATGTTTCATAGGAATGGATCGCTCTTCTCAAGGAACGTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCA
TATTTCCCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTTAAACCTAAGGGAGGTGATGGT

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FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK
IPYLEELHLLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLNDITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVRGLMCOAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPDIKNPCLTKDQQTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFDETPVCITETETAPL
RMYNPPTTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLKNNHSES
SSNRSYRDSGIPDSHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

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FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG
CAGCCCTGCCGGGCCACTTGTCTTCATGTCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCTCCAGCCCGGGTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTCCGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCCTCAGACCTCTCAGGAG
CCTCATGACCAAGCCCGGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTCCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG
GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTATATTTTTTTAGTAGAGAC
AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC
AGGCTCCCAAAGTGTGGGATTATTAGGTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAA
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCCTATACA
TCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
GCCACCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAA

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FIGURE 386

MSARGRWEGGGRRACRGSIGLARAQGAERVTSSEQRPAMASIGLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLOPL
SLRVGMLGEKLEAAIQRSLSHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHDTASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCFGEFDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSCILIPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRDPPPTSGSQSVGL

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

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FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTC**ATG**GCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGG**TAG**TCAG
GCCGTCCAGAGCTGGCATTTCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGGA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACGTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAA
TTATATGAACACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 388

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPQDWIS
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:**Signal sequence:**

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

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FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATGG**CGTGGAGCCTTGGGAG
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
AATGAATTCTGTAAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT
TATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
CCCTAAAATTGAGAATGAATACGAACTTGGACTATGAAGAATGTGTATAACTCATGGACTTA
TAATGTGCAATACTGGAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTATTGTGTTCAAGTTCGAGGGTTTCTTCC
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
GGTCCCCTCCTGGATGGTGGCCGTCATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCTTCTCCCCTAG
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
TTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAGTGTGATTGCAGAAGA
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG
GCCCCAAAGCT**AGG**CTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA
AAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCATGATGTTTTCAGAAGTTGGC
CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG
ATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
GCTACACAGAGCACGGACTTTTGGATTCTTTGCAGTACTTTGAATTTATTTTTCTACCTATAT
ATGTTTTATATGCTGCTGGTGCCTCCATTAAAGTTTTACTCTGTGTTGC

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FIGURE 390

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551
><subunit 1 of 1, 325 aa, 1 stop
><MW: 37011, pI: 5.09, NX(S/T): 4
MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMVAVILMASVFMVCLALLGCFSLWLWCYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP GDSCSL
GTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

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FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCGATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCC
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCGGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAA**TAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCAAACCCACGCGTGTTCTGAAGGTGCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

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FIGURE 392

MRKHLSSWWLATVCMLLFSLHSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMLVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

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FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCTTGCTTCTC
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACCTGTTTTCAAAAACCAACACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**TGA**ATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTTAATTAATGTCAGTATTTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATTGTTAAAAACAGAGAGGGATG
CTTGGATGTAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGGTAAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTCAATTTCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAA
AAAA

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FIGURE 394

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002
><subunit 1 of 1, 206 aa, 1 stop
><MW: 23799, pI: 9.12, NX(S/T): 3
MNFQQRLQSLWTLARPFPCPPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN
RTVEVRTLKSFSTLANNEFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL
```

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

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FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTATTTTT
TGAAATTTCACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGGT

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FIGURE 396

MFRSSLLFWPPLCLLSLFLLLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGGCGCCTTGGGGACGGGCAGTTCCCTG
TGTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCTATCCTTTTTTAGAAACACAAAT
TGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCACCCAGCAAGAGTCCCTCAG
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCGCAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAAACTGGCAGGCTGTGTATTCTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTATATGTGCAGATGGAAAAC**TGA**TGCCAACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

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FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGVKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPFLETQI
GPPEVALTTDEKSI SVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRIHVGKEKHHPANLILYGNFEDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDPKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQAAALAVLGPQTLQYSYTP
QLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526**Tyrosine kinase phosphorylation site.**

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

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FIGURE 399

CCGGCG**ATG**TCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAACAGTGTGCAACAGGGGAC
TATTCAATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTTCACAACCACTCCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTTCAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

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FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRLDRVEPVTTTSVATGDYS
ILMNVSWVLRADASI RLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVI PVTGDSEGATVQLTP
YFPTCGSDCIRHKGTVVLCPQTGVFPFLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTCGKSEGSPSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKQQVSAGKRSQACHDGCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

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FIGURE 401

GGGAACAGGGAACTATCAGCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG
GGACCTTTTTCGGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCCG
GGGCCCCGCCGCCCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTCTCTCCAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTCTGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTTGAGCTAAATAGCAATTC
TTTGGAGTCCTATGAAAATGTCATGCAGAGTTCCCTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAACAATC
CGCATCTTGGGCTTTAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCAATTAGAAAACGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGATGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTTCTTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTTCTGGTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCAGAAAGGCATTCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTCTGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAACAAAAAAATTA AAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAAATTATTTTATGAATTTACTGT

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FIGURE 402

MDRDLRLQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRVD
NIEIQKFISKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGSNLKA
IEDFELALENCPTHRNARKYLCQTLVERGGQLEEEEEKFLNAESYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKKRRKSTSSSS
VSSADESVSSSSSSSSSGHKRHKHKKRNRSESSRRRHSSRASSNQIDQNRKDECYPVP
ANTSASFLNHKQEVKLLGKQDRLOQYEKTOIKEKDRCPLSSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEEGIVIIDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

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FIGURE 403

CCGAGGCGGGAGGAGCCCCAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTTCCGAAC TGCCAGCTCAGAATA
GGAAAATAA CTTGGGATTTTATATTGGAAGAC **ATGG**ATCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTT CAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTT CAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCAT TGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTCCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCTTGCCAAC TGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATT CAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAGTGGTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCTTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTCTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGACACCCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAAACGATGAAACTGCAAAA

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FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVYK
VLATLGLILLTAYFVIQPFSPPLAEPVLSGAHTWRS LIHHIRLMSLPIAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPI PANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFVFTHL
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC
GTCTCCTCCTGTCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
CAGCGGACGACCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCCGCGTCCCGGGGATGCTCAG
TAGCCCCGTGCCCGGCCCGCGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAGTAGTC
ATGGTGCTGTGGGAGTCCCCCGGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
CCCGTCATGCTACTCATCGTAGCCCCGCCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGAAGTGCCTGCTG
CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCCTCTGTGACACCAACACCTGTAAA
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGCGTCTGTGAGTTCAAGTGAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGAGAGCTACCAGAATGAGTGTACCTGCCACAGGCTGCATGCAAACAGCAGAGT
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAACACTACAACACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGTCTGTACGATTTTCAATATGTCTTAAATCGCAGCTGTG
ATTGGAACAATTGAGATTGCTGTCATCTGTGTGGTGGTCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTTACAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
AGGGAGCATGTTTACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCCTGCATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTTCTTTCCCATGTATTTGTTATATATAATAAAATACTCAGTGATGAG

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FIGURE 406

MVLWESPRQCSSWTLCGFCWLLLLPVMLLIVARPVKLAAFPTSLSDCQTPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTTTK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY
TGQHCEKKDYSVLYVVP GPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTRASTRLI

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FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCCATTTGCAATTGTTTAACTACTTAGAAAATGAAGTGTTTCATTTTTAA
CATTCCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCACGACT
CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCAGAGGAGGCCGACGTGCC
CGAGCTCCTCCGGGGGTCCCGCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGGAATGCGCAGGAATAAAAAGGATACTCACTGTTACCATTCCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCACCAGTGCAACCCACCCAGATCTGCA
TCAATACTGAAGCGGGTACACCTGCTCCTGCACCCAGCGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTCTCTGGAT
CCTATTCTTGATCATGCAACCCTGGTTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAAACCTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACTTGAGGAAGATGGCGTTCATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCTCTGCCAACATGAGTGTGTGAACCAGCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCAAATGCAAGCCACGACCCGCTACCCCTG
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCACTCAACTTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTGCGAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTCTCTGCTGAACGTTTCCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTA
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCGAGTTCCTATGACACAGTTATCAAA
AAGTATTATCATTTGCTCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTTCGGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTCACTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGGCTTTTTCGCTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTGTAGAGAATGTGTTTCAAACCATGC
CTGGTATTTTCAAACCATAAAAGAAGTTTCAGTTGTCTTAAATTTGTATAACGGTTTAAATTCT
GTCTTGTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCCAGTGTTTTCTTT
GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCAATTGGATTGGAATGCAGAGGTCT
CCAACTGATTAAATATTTGAAGAGA

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FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYAAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGS LICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFTILYRDMDVVSGRSVPADIFQMQAATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCGCGGCTCA
GGGAGGAGCACCAGCTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
TCGCTGGTCCTGTTGATGCCTGGCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCTTACATTGAAGCTGGG
AAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCAGGACTGAACATGAAGAGT
TATGCCGGCTTCCTCACCCTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTGACAAAGTAACATGACCTTGCCT
GACAGAGACTTCCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
GGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
TTATACAGTGCCTAATTCAGTTTTTCCAGATATTTCCCTGAATATAAAAATAATGACTTTTTAT
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCTC
AACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG
CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT
CAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
CAGACTTTTAATGATGGAACATATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACCTGGAC
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCAG
GAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
TACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT
CCTTATGTTGGATAACTACCTTCCCAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTGGGGGGAGATGTTTACT
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTTA
ATTTCTTCTAAGAGTAAGTGAAGAGTGAGTTGTAAACAAACAAAGCTGTAACATCTTTTCTG
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAAATATTATTGGATAAGAATAGCTC
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTGGGGAAAAGATTCTCAAATGTATAA
AGTCTTAGAACAAAAGAATTCCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

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FIGURE 410

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSLV
GPFPGGLNMKSYAGFLTIVNKTYNNSLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVTSNMTLRDRDFPWTTTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFFQI
FPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNVREVKINLNGIAIGDGYSDPESIIGGYAEF
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGTGCSNYY
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKFWLTEIMNNY
KVLIYNGQLDIIVAAALTERSLMGMDWKGSSQYKKAEEKVWKIFKSDSEVAGYIRQAGDFHQV
IIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

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FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCAA
GCGCTTCGCGTCTTCTGTCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCCAGCTCACGGGCCTCAAGGAGCTGTGGCTTACCACACAGCGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCTTCTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCCTCAGCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGAG
GCCGCCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCCGAGGGGCGAGGCTAGCTTCTCCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCCAAGAAAGTTAGCCAGATGGAAGGTGTTAGGGAAAGGTGGGCTGCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCTCCAGCTGGA
AAGGCCAGGCCGAGCTTGCCCTCTTCAGTTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTAAATCAA
AAACAATTTTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAGCTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAGCAGCCAGACGT
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTCTCTGGGAGGGAGGTTTTTTGTTTTGTTTTTGGGTTTTTTTGGTGTCTTGTCTTTCTCTCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCGGATGAACGGTGCTCCATTGCGACCTCCCTCCTCGTGCTGCCCTGCCTCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTCCGGAATGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGCACACAGCCAGTCCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCTTAGATCAATCACGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

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FIGURE 412

MRQTIKVIKFIILICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSIGIPDPTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAACCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTTCAACTCCAGAGTTTCAAGATTTTC
ATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCA
AAACCTTTGAATTCACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAATGACTTTGACACCA
TGCTTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGAGGTGGGGCAA
AAATACAAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT
TCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAACAAAACTGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGGCGTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCTTATCTTACAATTTGTTTGGCATACATCAGTGGAACACTTTTCAAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCAGAATTCATTTGACTACTCAAATACTGTAATGA
GAACATAAAATGGAGCATGTACATTTCAAGAGTGTTTTACATTTCAACAGGATAAAATCTATT
TGCTTTTGAACAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGCCAATAATATCTTAACAGACG
AGTTGTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAACCTCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTTGCTTAACAACACACACCTTGGAAACACTTGGATCTGA
GTCAAAATCTATTACAACATAAAAAATGATGAAAAATGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTATACAATAAATTTGTCTGATTCTGTCTTCAGGTGCTTGCCCAAAAGTATTCAA
TACTTGACCTAAATAATAACCAATCCAACTGTACCTAAAGAGACTATTTCATCTGATGGCCT
TACGAGAACTAAATATTCGATTTAATTTCTAACTGATCTCCCTGGATGCAGTCATTTTCACTA
GACTTTCAGTTCTGAACATTGAAATGAATTTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTAA
AAAAATTTCAATTCAGCTTGAAACATATTCAGAGGTGATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCTTTAAACCTAAGGGGAAGTGGTTAAAGACGTTTATCTCCACGAATTTAT
CTTGCAACACAGCTCTGTTGATTGTCAACATTTGTTGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCACAGGGTTAGGAAAACAACCCAAGAACAACCTCAAGAGAAATGTCCGATTCACG
CATTTATTTATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTTGATTTGCTTTTATGAAAGCTACTTTGACCTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTTCCACCA
GGTATCATAAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAAAACCTTCGAGCTGCTATTAATGTTAATGTTATTAGCCACCA
GAGAAATGTATGAACCTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATTAATCCACAGTCTTGGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTAATAATAA
AAATGGTTATTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAAAGGTGTTTATCCCAGGATTGTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGAATCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCTGTCTCTACT
AAAAATACAAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAAAACATCCTCATGGCCACAAAAAAGGTCTAATTCATAAATTTATAGTACATTAATGT
AATAATAATTATACATGCCACTAAAAAAGATAAGGTAGCTGTATATTTCTGGTATGGAAAAA
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAAACTAATTGTGGTTTTTGGCCATTGAAA
TGGCATTGAAATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTTGGGTCTGG
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGATTTTCTATAATGTTTGAATTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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FIGURE 414

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ
QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLPHLKTLI
LNGNKLETLSLVSCFANNTPLEHLDLSONLLQHKNDENCWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDNLNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRLSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMVGWSDSYTCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVIMLVGLAVAFCCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHNNLFHENS DHII LILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLEFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

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FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCCTCCCCCGC
TTCCCTGTTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGGCTGACAGT
CGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCACTGCGGAGACCCGGGGCTTCAGGAGCCGGCCCGGGAG
AGAAGAGTGC GGCGGGGACGAGAGAAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCAGCCCTGGCATCCAGAGTACGGGTCGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTCCTGGAGGGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCTTGGTCCGGGACAGCCGCACCTCCCCTGCCAAGTGCACCTGGCTCATCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGCTCTCTTACAGCCAAGATTGGCTGATGTGCTTGCAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCTCCCTGCCCTTGAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGCTGGACCCCATGATGGCGGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTGG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCACCTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGCCAGGCTGTTGTGCTCCTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTCCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCAATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTCGCACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCAGCTCATTGCCCAGGGTGCCATCCCACCTGTAGAAGACTTCTTACAGAGAATCCTAATGATA
ACTCAGTGTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCGCTCGTCAGCGGGGCGGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGCTGGGGCTTGTCCCTCGAA
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAGATGGGGAGCAGGCACCCCACTGCCATCA
AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGAGGCCCTGCCAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGG
CTCTACTGAGGCCTCTCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCTCC
ACCACTTCTCTCCCTGTCCCTGGATTTAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACCTGCTCCCCACGCCACCACCTTTGGGTGGCTGTTTTTAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

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FIGURE 416

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHPDRIIFPNHACEDPPAVLLEVQGTIQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSH PQSCHWLLDPHDGRR LAVRFTALDLGFGDAVHVYDG
PGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRMLMRR LVRRLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTG PAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRL LPSLGPPGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT
```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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FIGURE 417

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTCCGAGGAGAGCACCCGGAG
GACGCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG
AGCCTCCCTTTGCCGCTCCCTCCTCTGCCCCGCGCAGCAGTGACATGGGGTGTGGAGGTAGATGGGCTCCCG
GCCCCGGAGGCGCGGTGGATGCGGCGCTGGGCAGAACGAGCCGCGATTCCAGCTGCCCCGCGCGCCCCGGCG
CCCCGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC
GCCCCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCCTAGACCACCACAGCTCAG
CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCATGGCCAAATG
ATTGAGAAATTACCTTGTGCTGCCCTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATACGGTGTGCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAGACAACGCTCTGTGGCACACTCCCGTCCCTT
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCAGCCCTGAGCACATGGAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAACCAACAGAATCCAACCTTCTGCTCTGTAGACCAAGGACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTGCCCCGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGGTGATTGTGGTG
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAGGGGCCCCGCGCAGGATCCAGTGCCATTGTGGAAAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTGAATGCCAGTGAG
AGGGAGGTTGCTGCTTCTCCAATGGGTACACAGCCGACCCAGAGCGGGCCCTACGCAGCTCTGCAGCATGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCCGAGAAACGATGTTGTGGAG
AAGATTCTGTGGGCTGATGGAAGACACCACCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCG
CTTAGCCCCAGCCCCATCCCCAGCCCCAACCGGAAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAGGGCTTCTTCGTGGATGAGTCGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCCCTTATTACCAAAGAAAAGAGGACACAGTGTGCGGCAGCTACGCCTGGAC
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTGCAATTTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTGTTTGGGGTGTGTGTGTGTTTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAGAATATGGCCAGTGCTTGAGTCTTTTCTCCTTCTC
TCTCTCTTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACCTGTTGTGAA
ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCTTCTTATGTATTTCAAGATTATTCTG
TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTTATAAATTTTCTTAAGATTAAAGAAATTTAAGA
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAAGATGCTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAACTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTCTGGAACACATTGCTGCACCTT
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCCTTACCAAT
ACTTTAATTAATAAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTTA
AAAAAAA

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FIGURE 418

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEKLPAAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTEDEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPGTAFPRPEHMETHEVPSSSTYVPGGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVNVHQGGPHRRHILKLLPS
MEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL
ETDKLALPMSPLSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRC DSTSSGS
SALSRNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTL LDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

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FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACCGCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCAG
AAGGGGACAAGACAGCTGTTAGGCTCAGCAGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCCTGCATTTCAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCAGTCTGGGCTCTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAAGTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGGCGGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTCTGTACCATTTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTTCACCGGCAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTTCCAAACATGTTGAATTTGTACAATTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCAGACAGTGAATGCCTACTACCTTCCAACATAAGATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCTGGTGGCAGAAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCCACAGCCCTGCCCCGCTTCCGCGTGTGGGCACTCTCTCAACTCCCGTGACTTCCTGCGG
CACTTCGGCTGCCCTGTCCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCGGTGTCAACCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCTATAGGAAGGAGTCTGCC

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FIGURE 420

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANЕКVLTAYLDYM
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES
AQEKLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSEFFQNMLNLY
NESAКVMADQLRKPPSRDQWSMTPQTVNAYYLP TKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:

amino acids 32-57

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FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACGATGTTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACC GCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA
GAAGATCCGGCACCACTCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACGGGCAGC
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCTCGGGAAT
CACAACCTGGGTACAAGACATTTGCCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCTGCACTGTCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTACAGTGAAGCTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCTGCGG
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCGGGACCCCCCTGCCTTCCTGC
TCACCCTACTCTGACCTCCTTACGTGCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCTACTCTGACCTCCTTACGTGCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 422

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLEFVACLSLGGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTRHRLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTGGATGCT
GCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAACCTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAAGATTA
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTTAGGGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCCTTCTTTTCCTT
TTTCTTCACCTTCATTTTCAGGCTTTTCTCTGTCTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965
<subunit 1 of 1, 175 aa, 1 stop
<MW: 19330, pI: 7.25, NX(S/T): 1
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD
ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWESSTD
VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:**Signal peptide:**

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 425

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTGG
CTGCTCCTGTGGGCTGCGGCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGT
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTCCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACCTGTGTCAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTTATAACCACCGGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCACCCAAGGCTTCTGTAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATT
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQH
YRALQQQLQRDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSGKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTGTTATCTTCACTA
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG
AGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 428

MGVEIAFASVILTCLSLLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
G TTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAGTCAAATTAAATTCTTTCCAATGCCCCAACTAATTTTGAGATTGAGTCAGAAAATA
TAAATGCTGTATTTATA

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FIGURE 430

><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

Important features:**Signal peptide:**

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

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FIGURE 431

GCGTGGGGATGCTAGGAGCTCGAAGGTGGTGGTGGGCCTCTCGGTGCTGCTGACGGCGGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCCAAATTCGGAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTATTT
TGACTGAGCAACTTGAAGCAGAAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCAATCC

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FIGURE 432

MSRSSKVV LGLSVLLTAATVAGVHV KQQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

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FIGURE 433

GAATTCGTGTCTCGGCACCTCACTCCCGGCCGCCGGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
CGCTGCCGCTGCTGCTGGGCCTCTTCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA
AGCCTTACCCGCTATTTCCCGGGACCTTTCCAGGGAGCCTGCAAACCTGACCACACACCGCTGTATCCCTTCCTC
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTCACCAACCCAGCCTGGAAGACCACATACAGGAACGTAGCCATT
CCCCAGGTGACCTCTGTGCAATCAAAGCCCCTACCGCCTCTTGCCTTCAAACACACAGTTGGACACATAATACTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
TGGAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCCCTCAGCATAACCAGTGTGCAGCGTTTCAGACAATGGGTCGTATATCTGTAAGATGAAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCCCTCACTTTACTAAGCAGCCTGAGAGC
ATGAATGTCACCAGAAACACAGCCTTCAACCTCACCTGTGAGGCTGTGGGCCCGCCTGAGCCCGTCAACATTTTC
TGGGTTCAAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGGCGTGTAACTGTTCCAGGCCTGACG
GAGATGGCGGTCTTCAGTTGTGAGGCCACAATGACAAAGGGCTGACCGTGTCCAGGGAGTGCAGATCAACATC
AAAGCAATTCCTCCCCACCAACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
CCTGGTTTTGATGGATACTCCCGTTTCAGGAATTGCAGCATTGAGGTCAAGGAAGCTGATCCGCTGGGTAATGGC
TCAGTCATGATTTTTAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTGGTGTTCCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCACGACTGAA
GGAGCCCCATCAGTAGCACCTTTAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGTGTGCAGAGTGCAGGG
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAGGATTGCAGCCGTCAACAGAGGGGAGTTGGGCCCTTCAGTGATCCAGTGAATATTTATC
CCTGCACACGGTTGGGTAGATTATGCCCTCTTCAACTCCGGCGCTGGCAACGCAGATCCTGTGCTCATCTC
TTTGGCTGCTTTTGTGGATTTATTTGATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAGAAATCCTTC
TGTCGGCGAGCCATTGAACCTACCTTACATAGCTTGGGAGTCAGTGAGGAACACAAAATAAACTAGAAGATGTT
GTGATTGACAGGAATCTTCTAATCTTGGAAAAATCTGGGTGAAGGAGAGTTTGGTCTGTAATGGAAGGAAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTCTTCACATCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTGCATGAAAGACTTCAGCCACCCAAATGTCATTGCACTTCTAGGTGTG
TGTATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
ACTTACTTACTTTATTTCCGATTGGAGACAGGACCAAGCATATTCCTCTGCAGACACTATTGAAGTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTTGCGGACTTCGGCCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
CAAGGCCGATTGCTAAGATGCCTGTTAAATGGATCGCCATAGAAAGTCTTGACAGCCGAGTCTACACAAGTAAA
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCGAAGACTGCCTGGATGAACTGTAT
GAAATAATGTACTCTTGCTGGAGAACCGATCCCTTAGACCGCCCCACCTTTTCAGTATTGAGGCTGCAGCTAGAA
AAACTCTTAGAAAGTTTGCCTGACGTTGGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC
TGCATCCCCGCGCTGCCATCAGTGTGGTCACAGCAGAAGTTCATGACAGCAAACCTCATGAAGGACGGTACATC
CTGAATGGGGCAGTGAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT
GTTTTACCAGGGGAGAGACTTGTAGGAATGGGGTCTCTGGTCCCATTCGAGCATGTGCCCCCTGGGAAGCTCA
TTGCCCGATGAACTTTTGTTTGTGCTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGGGGGA
GACATTCCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT
CCTTACCAGTGAACCTCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATAAAAATACATAA
TATATATTTATTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAATAAAACATTACTTA
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTTCAACTTCTTTTCTTTTCAATTACTATTAAATGTAAAAATATTTGTAAAAATGAATGCCATATT
TGACTTGGCTTCTGGTCTTGATGTATTTGATAAGAATGATTAATTTTCTGATATGGCTTCATAATAAAATTGAA
ATAGGA

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FIGURE 434

MGPAPLPLLLGLFLPALWRRRAITEAREEAKPYPLFPFGPFGSLQTDHTPLLSLPHASGYQPALMFSPPTQPGRPHT
GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNCISINVPNIYQDTTISWWKDGKELLGGHHRITQFYPD
DEVTAILASFISITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE
PVNIFWVQNSSRVNEQPEKSPGVLTPGLTEMAVFSCAANDKGLTVSQGVQINIKAIKPSPTTEVSIRNSTAHSI
LISWVPGFDGYSPFRNCISIQVKEADPLNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQQDGELVGYRISHVWQSAGISKEELLEEVGQNGSRARISV
QVHNATCTVRIA AVTRGGVGPFS DPVKIFIPAHGWVDYAPSS TPAPGNADPVLIIFGCFCGFI LIGLILYISLAI
RKRVQETKFGNAFTEEDSELVVNYIAKKSFCRRRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS
VMEGNLQEDGTS LKVA VKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGI PKPMVILPFMK
YGD LHTYLLYSRLETGPKHIPLOTL LKFMVDIALGMEYLSNRNFLHRDLAARNCMLRDDMTVCVADFGLSKKIYS
GDYYRQGR IAKMPVKWIAIESLADRVYTSKSDVWAFGVMTWEIRTRGMT PYPGVQNH EMYDYLLHGHRLKQPEDC
LDELYEIMYSCWRTDPLDRPTFSVLRLQLEKLLES LDPVRNQADVIVNTQLLESSEGLAQGPTLAPLDLNDPDC
SIIASCTPRAAISVVTA EVHDSKPHEGRYILNGGSEEWEDLT SAPSAAVTAEKNSVLPGERLVRNGVSWSHSML
PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

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FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCGGGCAAGGAT
CCAAGCATGGAATGCTGCCGTCCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTTCTG
CTCCTGAGTTCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCCGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAGGTCCTGATCACTTATATCTGGAAACC
AAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACCTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGGCATCCAG
AGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTGTACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAACCCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGTCAGAGGAG
CCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATATTTGAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACCTAAGTGAATCATCTCACCAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

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FIGURE 436

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847
<subunit 1 of 1, 525 aa, 1 stop
<MW: 58416, pI: 6.62, NX(S/T): 1
MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSLKCQAK
GTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFI FYQPIIHRWRETDFPCSATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKEKLPVEAK
LPWFKQAQELEEAAVSEEPS
```

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTACAGGACATTCGC
CCCTGTGTGCCACCAACCAGGACTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCACCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAAGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

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FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQGGSGMEH
RNHLCFCDLYDRATSPPLKCSLL

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FIGURE 439

GTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTTCAGAACAAAGCTTCCCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAGAAGTGGAGTGTGTCAGGGACGGCAGTATCTTTTGTGTGACCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCACTGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTCACTGGCTTGCCCTCCTAGCCACAGCAGGCTGCTTGTGCTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGAACCTCCA
AGGATGAATGTAACCTGGCGCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCATCACC
CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGGCCCGGATGCCCTGCG
GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCAGCTG
ATTGAAGTGGATGAGGGAACACAGCAGTCAATGCCTGCCACCTGCCTGAGAGCCACCCCAAAGCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACCTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAACACC
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC
CAAACCATCATCGTCAACCAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCCACGGGT
ACCTGGGCCAAGGATGGGTCCAGTGTCAACGGCTACAACAAGACGCGCTTCCCTGCTGAGCAACCTCATCGAC
ACCACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCGACCCGGGGCAGCGGT
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTCAACATGGAGCTATCCAGTGGTTCATCCCTGGGGC
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGCGCTGAGGACGAAGG
GTCTACCACTGCATGGCCGAGAACGAGGTTGGGAGCGCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCGAGACCCCAACGTCAGTGGGGCTGCTTCCCGAAGTGT
CCAGGAGAGAAGGGGCGAGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTCGCCCCGACCTCCAAGACAGAC
TCATATGAAGTGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC
CGAAGCAGGTCAAAATTCCTCTGACGATTGGACCATCTCTGGCATTCAGCCAACAGCAGCCGCTGACCCCT
ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGAGAGGGCCAGACAGCC
ATGGTCACTTCCGAAGTGGACGGCGGCCCAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
GACCCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCAGCGCGCCTCTCCCCCCAGAAGCTCCCGACAGG
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTCAT
CAGTCCCTCCGTGTGGAGTACAAGAAGCTAAAGAAGTGGGAGACTGGATTCTGGCCACAGCGCCATCCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGGCTACAGCGGTGCGGTGTACGAGAGG
CCCGTGGCAGGTCTTATATCACCTTCAGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGT
GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCTAC
GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTGAGCAACGTGATGATCTGTGAGACCAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTTCGACTGCCACCCCAACTCTGGCCCCACACAGCCGCCCTTCTGAAACC
ATAGAGCGGCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGGTCTGCT
CTGGGCTCCATCGTTCTCATCATCGTCACTTCTATCCCTTCTGCTGTGTGGAGGGCCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTCCACCTCCTGCCCCGATATACTATGGTGGCATTGGGAGGACTC
CCAGGCCACAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCTGCTGAGGCAGACCATCTTGGCAATGGATATGACCCCAAAGTACCAGATC
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACACTGCCCGACGACTCCACTCACCAGCTG
CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCTGCTGCTGTGGGCCAGTCAAGGGTGGAGAGGCC
CCCGACAGTCTGTCTGGAAGCAGTGTGGGACCTCCATTTCACTCAGGGCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCCTAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCCACTGGTGGCTGTGCTTTTGAACACCACT
CTCACAATTTAGGCGAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAAAGAGAAAA
AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCATAATTTATATTTATGCACTTGTAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTTACCCGTTGAGTTGGAGAGGGAAAATAAAGAAGCTGCCA
CCTAACAGGAGTCAACCCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGGAGCA
TGAGGGAACAGCAAGGGGCACGGTATCACAGCTGGAGACCCACACAGATGGCTGGATCCGGTCCGTACCGGAA
ACATTTTCTAAGATGCCATGAGAACAGCAAGATGTGTACAGCACTATGAGCATTAACCAACCTCCAGAAT
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACCTCTAATAAATGTTTAGTCTTCCCTGTAAAA

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FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGAIVILY
NVQVFEPPEVTMELSQLVLPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCAENEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGEGKGQGAPEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGASPDHGRSLPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGSYKFRVRALNMLGESEP
SAPSRPYVVSIGYSGRVYERPVAGPYITFTDAVNETTIMLKWMIYIPASNNNTPIHGFYIYYRPT
DSDNDSYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVLIIIVTFIPFCLWRAW
SKQKHTTDLGFPRALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTLPPDS
THQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHS GPPCCLGLVPVEEVDS PD
SCQVSGGDWCPQHVPVAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

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FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGC**ATGG**CAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTCGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTATTATTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCTGGGAAACACTCTGAGATATATA
ACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCA**TAA**CTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

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FIGURE 442

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWWNGSEPLWVT
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLA AIYH
ERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

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FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCAATGAGGATCATGCTGCTATTCACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG
AGCAGAATAGGTACTCCACTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCAGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTG TG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTACATTAAAAAT
ATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRP

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCAATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCAACTTTGGATTGTAATAAAACAATTGAAACACCA

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FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCA**ATG**ACGCTCCTCCC
CGGCCTCCTGTTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCCGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGCGCTGCACCTGCGTGCTGCC
CCGTT**CAGTGTGA**CCGCCGAGGCCGTGGGGCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAACTGATGAACACATCCCCAAA

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FIGURE 448

MTLLPGLLFLTTLWHTCLAHHDP SLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWR YRVDTDED RYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLLVLR RRPCSRDGSGLPTPGAF AFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

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FIGURE 449

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCGCCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAAGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCACTCATGACTATGCCTTCAGTAGTGTGAAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACTGTCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTCTGTTTCACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTAAAC
CACTGATAATTCAGATTTGTTTCAATTAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCCGAGAAATGCCCCCTCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC
TGCACTCCTTGCTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAAACTGAACTATTGAAGTGACACACTCCTTTTTTCCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAAATAAAAGTAATCCCTGCTGGTTCATAGGAAAAAAAAAAAAA

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FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDCKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEEASNWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETQLQAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTTDNSDL
FINSIGIVPSVREKEDPEPSTDGTYYWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSSIILHDLRYLLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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FIGURE 452

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGMRLQEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

FIGURE 453

TTCGGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCGCGGGGGGGCGATGACCGTGCGCTGACCTGACTCACTCCAGGTCGGGAGGCGGGGGGCCCGGGGGCGACTCG
 GGGGCGGACCGCGGGGCGGAGCTGCCGCCCTGTGATCCGGCCGAGCCAGCTGAGCCCCAGGCCGCGGACACCGTC
 GCTCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCCTGAGGAGAGCTGGCTCGCGCCCCATGGGCGCGCTGCGC
 CTCTGGCCACCGCTGCTGCTCTGCTGCTGCTCTGCTGTCAGCGCCGCGCTCCGACCTGGGCGCTCAGC
 CCCCAGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACCTAC
 ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCTGTACCTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
 AACCTCAGCTTCTCTGCCAGCGCGGGAGTACCGAGAGCTGCTTTGGGGTGCGACGCGAGAGAAGAAACAGCAGTGC
 AGCTTCAAGGGCAAGGACCCACAGCGCTGTCTCAAACATACATCAAGATCTCTGCGCTCAGCGGCAGCTCA
 GTGTTCACTGTGGCAGCAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATCTTGAGAAGTTTACCCTGGCAAG
 GACGAGAAGGGGAATGTCTCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTCTACACTGGACAGTACAGAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCCGCCCCCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCAGCTTTTGTGGCTCAGCCTAC
 ATTCTGAGAGCTTGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTTCTCAGCGAGACTGGCCAGGAA
 TTTGAGTTCTTTGAGAACACCATTTGTGTCCCGATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
 CTACAGCAGCGCTGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCTTCAAC
 GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCTTTTCTATGGGGTCTTCACT
 TCCCACTGGCACAGGGAACTACAGAAGGCTTCGCCCTGTGTTCTTCAATGAAGATGTGCAGAGAGTCTTC
 AGCGGCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCTGACCCACCCGCTGCCACACCCCGG
 CCTGGAGCGTGCATACCAACAGTCCCCGGAAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCGCGTGTG
 AACTTCTCAAGGACACTTCTGATGGACGGGAGTCCGAAGCCGATGCTGCTGCTGACGCCACCGCTCGC
 TACCAGCGCGTGGCTGTACACCGGTCTCCCTGGCCGACACCACTACGATGCTCTCTTCTGGGCACTGGTGAC
 GGGCGGCTCCACAAGGCAGTGAGCGTGGGCCCCGGGTGCACATCATTGAGAGCTGCAGATCTTCTCATCGGA
 CAGCCCGTGCAGAACTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCTCACACTCGGGCGTAGTCCAG
 GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCTCGCCGGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTGCAAGCAGCTGACGCTCTACAGCCTCAGCTGGCCACCAGGCGGTGGATCCAGGACATCGAG
 GGAGCCAGCGCCAGGACCTTTCAGCGCGCTTCTCGTTGTGTCCCCGTCTTTGTACCAACAGGGGAGAAGCCA
 TGTGAGCAAGTCCAGTTCTAGGCCAACACAGCTGAACACTTTGGCCTGCCGCTCCTCTCCAACCTGGCGACCCGA
 CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCTCCTGCCACGTGCTACCCACTGGGACCTGCTGCTG
 GTGGGCACCCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCAGCAGCTGGTAGCCAGTAC
 TGCCCGAGAGTGGTGGAGACGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTAACCTCATTATCAGCACAC
 TCGCTGTGAGTGTCCAGCTGGTGGCAAGGCCAGTGGGGTGACAGAGTCTACTGGAAGGAGTTCTCTGGTG
 ATGTGCACGCTCTTTGTGCTGGCGTGTGCTCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA
 GTCTTCTGAAGCAGGGGAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGTGGTGTGCCCCCTGAGACCCGC
 CCACTCAACGGCCTAGGGCCCCCTAGCACCCTCGCTCATACCGAGGGTACCAGTCCCTGTGACAGACAGCCCCCG
 GGGGCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCAAAGACAGTCTCGTGGAGGTATCCCCAGTG
 TGCCCCCGGCCGGGTCCGCTTGGCTCGGAGATCCGTGACTCTGTGTGTGAGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCCCTCGCTCTGCTCTTCGTGGAAC
 ACGACCGTGGTGGCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCCTGGCCAAATATGGGGGCTCGCTAGGTTGGTGAA
 CAGTGCTCCTTATTAACCTGAGCCCTTGTGTTTAAAAAACAATCCAAATGTAAACTAGAGAGGAAGAG
 ATAGACTGGCATGCAGACACACGCGTCTTCCAGTTACATGGCCTCCAGGGGTGCTGGGGATGCATCCAAGATGG
 TTGCTGTGAGACAGAGTTGGAAACCTCACCAACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
 CCTGTCTCACTGCAGATTCAAGACAGCTTGGGCTGCGTGCCTTCTGCCCTGCCAGTACGCCGAGGATGTAGTTG
 TTGCTGCCGTCGTCACCACTTCAAGGACACAGAGGGTATGGTGGCAGTCGGGCCCTCACCAGGTCTCGGGCTC
 GAGCCAACTCTGAGCTTTCCAGCCTGTATCAGGCTGTGGCCACAGAGAGGACAGCGCGAGCTCAGGAGAGA
 TTTCGTGACAAATGTACGCTTTCCCTCAGAATTACAGGAAGAGAGCTGCGCCTGCCTTCTCCGTTGTTGCGTGA
 GAACCCGTGTGCCCTTCCACCATATCCACCCTCGCTCCATCTTTGAACTCAAACACGAGGAATAACTGCACC
 CTGGTCTCTCCCACTCCCACTTACCTTCCATCCCTCACCTTCTCCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGGCCCTGAATTTATGTGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCATTTTTTAATAAA
 GTCTGAAGAATACTGTTTAAAAAATAAAAAA

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FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGGDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRDD
GFPFNVLQDVFTLSPSPQDWRDTLFGVFTSQWHRGTTEGSACVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFGLTGDGRLHKAVSVGPRVHIIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQQLATRPWIQ
DIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLLLVTGTLGEGFQCWSLEEGFQQLVASYCPEVVEDGVADQTDGGSVPVII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGACGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGGCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTCTCTCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCTTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCACTTGCGCCAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAAGTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTCCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTCAAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAGGGGGCCAGGGAGTCAAGAATATAACCGTGTTCCTC
CAGGGTTTAAAGCCGGCCATGCCTTCCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCCTTGCCCACAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCAATCCCTCACAGCCTGACCCTCCTCATTCCATCA
GATCTCGTGCCG

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FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRWWVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

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FIGURE 457

CCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGGCCGTCGGCCCCGGCTCTGGGGGCGCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCC
CTTGTGACCCCCACTCCAGCAGGGACCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGGAACACACCGAGGACGGCTCAACATTCATTAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCCCTCGGGGAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCCTT
GAGGCCCCCTCGGTGCGGATCCTCTGACCCTCTAGACTTTCAGCATCACAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTACCCATTCGACATGACTCGCACCCCGTGG
GCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCTCAC
GAGAAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
CTGCTGACCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTTCAGTGACACGG
AACTGTCCGGTACCTTTGAAGAGGGCCCCCTTCCCCTGCAATTTCTGTGCTCACCAAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGATTGATAACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAVAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTLWLGGAFCPLRAEILACPVSNDPDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPBGYEIAYHRGSELVG
WAEGRWNNQSIDLNHNFAADLNTPLWEAQDDGKVPHIVPNHHLPLPTYITLPNATVAPETR
AVIKWMKRIPFVLSANLHGGEVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTGPDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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FIGURE 459

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAAGTGAAGTGAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCCTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 460

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYFPRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

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FIGURE 461

AGCAGGAGCAGGAGAGGGGACAATGGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGT CATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTTCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTCTGACTTTCTCCTTGGAACTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCTTTTAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCTACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGTTGTATACTGCACATGACTT
ACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

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FIGURE 462

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPVSGVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAALF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL
```

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 143-162

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FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTTCAGCA~~CC~~ACTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAA~~CT~~CA
CCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

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FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMYTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

FIGURE 465

[illegible]

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FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTPLL LLLLLLLLLLWVPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ
ELLLELEKNHRL LAPGYIETHYGPDGQPVVLAPNHTDHCHYQGRVRGFPDSWVVLCTCSGMSGLITLSRNASYYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGAACLSNAPDPLPVPPALCGNGFVEAGEECDGCGPGQECRDLCCFAHNCS
LRPGAQCAHGDCCVRLKPAAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWGDGACPTLEQQ
CQQLWGP GSHPAPEACFQVNSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRCRKNAFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPPLPGAGLAWCCYRLPGAHLQRCSWGCRRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLFAVSPDPQADQVQMPRSCLW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metalloproteinases, zinc-binding region signature:

Amino acids 342-352

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FIGURE 467

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAAACATGCAGCTCGGCACTGGGCTCCTGC
TGGCCGCCGTCTCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTACCAGTGCACGG
GCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTACCACTG
CCACCCGGGTCTCTCAGCAACACCGAGGATTTGCCTCTGGTCACCAAGATGTGCCACATAGGCT
GCCCCGATATCCCCAGCCTGGGCCTGGGCCCTACGTATCCATCGCTTGCTGCCAGACCAGCC
TCTGCAACCATGACTGACAGCGCTGCCCTCCTCCAGGCCCGCCGACGCTCAGCCCCCACAGCCCC
CACAGCCTGGCGCCAGGGCTCACGGCCGCCCTCCTCGAGACTGGCCAGCCCACCTCTCCCG
GCCTCTGCAGCCACCGTCCAGCACCGCTTGCTCTAGGGAAGTCTTGCGTGGAGTCTTGCCCTCA
ATCTGTGTCGGCTCCAAGCTCTGGGGCCCATCGTGCCTGCCGCCCTTCAGGTCCCAGACCTCCC
ACAATAAAATGTGATTGGATCGTGTGGTACAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYYSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

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FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACCTTCCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATGT
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTTGGTCTCATTTTA
AACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCGTT
CTCAGCTCATTGCAACCTCTGCCTTTTTTAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAACACTTCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTGTTGTGTAC
AGGATTTTGTGTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACATGTGA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

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FIGURE 470

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPFIHFKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL
```

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

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FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTTCGGGAGGGTTTCGTCATCAACCTCCTTCCCGCAAACCTAAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
ACCGGGTTGGCGCTGCCCGAGTGGAAACCGACAGTTGCGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCGCGGTT
GTTGTTCACTGTTCGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTTCGCTTCTTCTCCTCTTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
GGTCTTACCGAGACCGATCCGCAGCGTTTGGCCCGGTCTGCCTATTGCATCGGGAGCCCCGAGCACCAGCGGAA
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGGCGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTACCGACCAGTTTCAGTTCGCCGATGGGAAACCCGGAGACCAAACTCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCA
CAGGTGGAAGAACTTGGACTTCTCAAGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
GCCAGAAGCTTACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTT
CGATTTTCCATTTTATGGCCACTTCTTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCAGTGTATCCAGAAA
TTCAACTGTGAGATATTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCAGGATAATTA
TAACCTGGGAAGCTTACATTTCCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAGTCCGACTGTCCGATGCATTTGTCTGTGTTCA
CAGGATCCAACAAATTTCCCAATGTTGGAAGAAGAAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
AATTACCAACATTTCCGGCTGTGGAGATGACCCATTACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT
ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGGTCCCTAACTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGGAACCTCCACGCTGGCCTCATCATTTGGAATCCTCATCCT
GGTCTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA
AGTTGAACCAAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCATAAATTTCTAGGACAGAACAACACC
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACACACACAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
AAACTAAAACCTTATACAAGATAACATTTACACTGAACATAGAATTCCTAGTGAATGTCATCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
GGATCAGAAAAAAAATCATAATAAGCTTTAGTTTCATGAGG

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FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVQTQAFPHTEEEVEVD SHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSFDTLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS
ASRDLWVNIDQMEKDKVKI HGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIY EYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTT VGATTTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAGTGTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAACTTGTC
GGCTTTCAAGACATGGAGTGTGTGCCTTGTTGGAGACCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTTCGAGGACATTCAG
TACAACGGCTCTGAGCTGTCGTGTTTTGACAGACCTCAGCTCCACGAATATGCCCACAGAGCC
TGCTGCCAGTGCCGCGGTGACTCAGTGCAGACCTGCGGGCCGGTGCCTTGTCTCCATCCATG
TGCTGTGAGGAGGCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCATGTTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACCTACTGGAGAAGACATTCATCTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGCT
GTTCCAGTCCAGTCTCATTTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCCTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTTCCAGAAATAATTTTCATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTGCGATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTGCCCAGAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTAAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCGTTCACTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGAATTGCCCTGCCCAAGTCACTGTCTTTTAACTTTT
AAACTGAATATTAAAATGTATCTGTCTTTCCT

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FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLRLHRFKEDWGFQKCKPCLDCAVVNRFAQKNC SATSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCMCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFTAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

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FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 476

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHRPSC
TTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGATTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT
TCCTTTTCTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGAGCTGGCTGCAAGGGGAACAGGGGT
GGTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAAATGGATGATCCCTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAATACACGATCAGCCCCAATCTTTTTTCCATATTAACTTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCAATTTTTGATGCCTCAGAAAATATTCGAACGAC
CTTTCAAATCAATCCTTTTTCTGGGGAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTCTGCAAGATGTAGGGTTTTAGTGGAAAGTATTGGACACCAA
TGACAATCCCCCTGAAGTATCGTATCATCTTTTCCAACCTCTGTGCTGAGAATTCTCTGAGACGCCGCTGGC
TGTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACTAACGGTCTGTGT
CTCCGACGTCAATGACAACGCCCCCGCCTTACCCAAACCTCCTACACCTGTTCTGTCGCGAGAACAACAGCCCC
CGCCTGACATCGGACGCTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCT
GCCGCCCAAGACCCGCACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTGCGCCT
CAGGTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGTGGGCGCCACAGACCGCGGCTCCCCCGCGCT
GAGCAGAGAGGCGCTGGTGCAGGCTGGTGTGGACGCCAACGACAACCTCGCCCTTCTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGCGGCGGAGCCGGGCTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCTGGTGTGCTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCG
TGTGTGGGCGCACAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGAGCCAAGCACAGGCTCGT
GGTGTGTGCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACCTGCTCCTGGTGGACGGCTT
CTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGCCAGGCCAGGCCGAGGCCGAGGCGGACTTGTACCCGTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCTGCTCTCTCTCTCGGTGCTCCTGTTCTGTTGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTCGGTGCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCTGTCCCAGAGCTACAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACAGTGAAGTT
CAAGTTCTTGAACAGTTATTTCCGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATCCACCTT
CCGAAATAGCTTTGGATTTAATATTCAGTAAGTCTGTTTTAGTTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTT
CTAAATGATAGTTAAGGTTTTAATCTTTCCAACCTGCCAAGGAATTAATTACTATTATATCTCATTACAGAA
ATCTGAGGTTTTGATTCATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGCTCTA
TTTAAGAAGGCATATCTACATTTCCAACTCATTCTAATCTATATATTCTGTTTGAACCATGTCAATTTA
TTTCTACATCATGTATTTAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTCTTATGTTAACTTTTGCTGATGTATAAACAGACTATGCCTTATAATTGAAATAAAATTATAA
TCTGCCTGAAAATGAATAAAAAATAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 478

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLEFLFWGVSLAGSGFGGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSITLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTDNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLLKPSVENFYILITEGALDREIRAENITITVTDLGTPRLKTEHNITVLV
SDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPQDPHLPPLASLV
SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGFSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIAQGPGRKGEENSTFRNSFGFNIQ

```

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCATGGGGACCTGTGCGGTTGG
GAATATTGCTTTTCCTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGGCCTTAG
AGAAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTTTTGACCCTTGCCCTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG
AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTGATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCTATATCGCTATT
AAACTTTTTTCTTTTTTTCTA

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FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
LGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMTATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLLKKQCETMLEEFEDIVGDWYFHHQEQLQNLCEGHVL
PAAETACLOETWTGKEITDGEEKTEGEEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

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FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAATGCGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGAAGAAGAAGGATATTCGCGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTGGTGGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCCATTTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAACTCT
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAATATGCTTTGTGAACCTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACCTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTGAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTTCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

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FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQNYPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAAACAGTGAAGTTTGTGTTGACTAAAAAAA

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FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

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FIGURE 487

CGGGGACGGAAGCGGGCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

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FIGURE 488

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGCGPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSFAFGEDGEDDLWTVRCGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL
```

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGATCACTGTGGTGCCCTTTTCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGCAGACACCCACCAT
CCAGTCTCTGGCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTCAGCATGCCCGGGGTGAGCAGCCATGCAGTTCGCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACCT
ATCTCTGCTGAATAACTACGTCTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAGCCTGGAAGGCTACACCCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTGACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG
CAACCACCTCACCTACTTTGTCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGTCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTGCTGCACTTCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCTGAACATCGCCTT
CCTGCTGAGCCCCGATTTCGAATGTCTCCTGTGCCCGGGTGCAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA
CGCGCTGCTCAGTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTCT
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTTCATGGGCTACGGCGGCCCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCGCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGCTACTGTGCTGGGCTCACCGTGTGCTGGGAACCACTGGGCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCGAGCTGTCTCTTCCACCATCTTAAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGGTCTGCTCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCTTCAGCTC
CTCCCAAACAACAGTAGTCCGGCCCTCCTGGCCTTGGAAATCCTCAGCCTCTCTGGCCCGCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGACCCCAGAGGCCACTGTGACCGCCAAGGGGCTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACCTTGTCTGCTGCTACCTGGGCCAGCTCGCCAGGGATGTGGGCAGAGACCA
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTCAGCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGGAAGAGTGTGACGTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGCTAGGGGC
AGGATCTCATTAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCTTCCCAAAGATTGGGAGGTTCCGCGGTTCCAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
GAGGAAAACGCTTCTTTCTCTCCAGCTGAATCAGCTGGATCCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCAGGTAGGCGTGAGAGTGTGGTTTTAAATTGCAAGCTCAGGCCATAGTTTCAGAGAATCACCC
TTACCCAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCGTTTCCAGAACGAACTAGGCGGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTGACAGACCCCATGCAC
CAGCTGGAGGGGCCGTAACTGCAGGACTGCGCCTACTGAGTGACCCATTCTCTCAGGAGGAAAGGCAAGACAG
CTTACACGSCCATTTGTCTCTTTTCCAATGCGGCGGTGCACTTTCGCTCTTGGGGGCTGCACCCAGACATAGC
TGGCACCAGAGCAGGGTGTCTCAGGTGGTGGTGTCTCAGGGCCCTGCCCGAGGCCACTGGGCGGTTTTGATGACCT
CAAAGGTCACAGGCAGAAAATAGGAGCAGGATTTCCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAAATAACTCCTTCACCAGGCACTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCTCAGTTTTCC
TATTTGTAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAAGAATTCAAATAAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

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FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQNATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGQHARGQHAMQFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNIAFLL
SPAFA MSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSLSVKSSVYGPCPTIPVFD SWENGTGFQNM SICWVRSPVH SVLVMGYG
GLTSLFNLVLA WALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQ HAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

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FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTTCGCACACGGGCTGCCCTGAGAGACATTTT
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCCC
TGAGAACCCCTACCTGATAGACCCAGAGAACC AAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTACAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCCTCAGCTACTGGCGAAAGCCAAGGAAGTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTGAAAAATACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTGAGATCAGGTATCATTTAGTGTTGTTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAAA

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FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTTLTDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCCAGAGAAAAGCTTCTGTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAACAACCTCATTAATGCTGCAAACTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACTTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTAGTTACACCTGAACCTGACCTGTTTCAAACAGGAATTTCCATCGT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCAGCTGACTGTTAAGAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATTAAGTTGTTGGACTCTAGTAC
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT
CATACCCTTGTATAATTGGAATTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTTGTGCAGGACAGTAAAT
AATGAAAACCAATTTCCCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
TATCCTTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTAAATGGTTATATAAAATTCATTGTATAGTTATAT
CATTATTTAATTAATAAACAACCCCTAATGATGGATATTTAGATTCTTTTAAAGTTTGTATTTT
CTTTTAAAGTTTGTGTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTCATATATCTCT
TTGTTTTTGTAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCTGCTTCTACAG
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAAATGGATTTATA

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FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSC TKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYR CIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIILTIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

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FIGURE 495

CCAGGTGCACAGCGCATCGCCCGAGGCTGTACCGCCCTGCCCCGCCACCCCAGCTGTCCTG
GACCCAGGGGACAGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAAGTACCACCTGCACCA**ATGGG**
GCTGTCCCGGAAGGAGCAGGTCTTCTTGGCCCTGCTGGGGGCCCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTTCTCCTCCTGGTGGAGGCCACCAAGCGTGCTCCTGCCACAGACATCAAGTTTGG
GATCGTGTTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCAGAGGCCACGATCGGAAAACACCCACGTTCTTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTGCAGCAGTCACCCAGGT
CCTGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCCCTCACCCA
GATCACGTTCTGTCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTCGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCCGCCGGCTGCCCTGCTCCGTACCCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTCAACCTGTGTCCAGCCAC
GCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGTGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCCTCCTGCACGAGGGCTAC
GGGTTGAGCGAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGAC**TAGT**GGGAAGGCGGAGGT
GGGCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCCTCCCGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGCCTCCACACCCACTTGGAGGGGTGAGACTGCAGTGGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAA

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FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVLEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTGVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVVWAKVVFVVLALVAVVGAALVQLFWLQD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTCACCTGTCTCAGGAACCACCTGAGCCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCTGGTTCGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTCATTG
CTGGTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTTCGCGCCCCAG
AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCTGGTGCAGAAGCACATTAAAGCTGTCT
TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCAGATCCGCTATTCCATGGTCAGTGTGC
CCACTGTCAACAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
CCATCATCCTGCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCACAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGGCCTCAACCTGGACATCACAGGGCAGCTGAGGTGCGATGACAACCTGCTGAACACCT
CTGCTCTGGGCCGGCTCATCCCGGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCTGCGGC
TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAAGTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGAGAAGCCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGAG**GGCAAGACCACT
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTGCCCCACCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAACAACCTTCTCTTGAGCTGC

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FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRHLKFIAGFGVRLAAANFTFKVFRAPEPLELTPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPEsqIRYSMVSVPTVTSdyISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVR LGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVF EKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

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FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAGC
CCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGCTCTTCCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTTGAGACTCATT
CCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGLTYN TTCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

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FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGGCTGCTGACATGTGTGCCTTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCTTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

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FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLQEGSQRRLRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLIFLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

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FIGURE 503

ACGGGCCGCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCAG
TCGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCCATGGC
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACAA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCCTTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAAGTGGTGAATACTAGGATA
TTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGATTAAAGTAGAAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGATATTCAAAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTATATTGCAGTTTTTGAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTAGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTTCGTTTCATAAGAGGTAAAGGTCAAATTTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

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FIGURE 504

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPQ
LKC VG GTAGCD SYTPKVIQCQNK GWDGYDVQWECKTDLDIAYKFGKTVVSC EGYESSEDQYVL
RGSCGLEYNLDY TELGLQKLKESGKQHGFASFSDY YKWSSADSCNMSGLITIVVLLGIAFVV
YKLFLSDGQYSPPPYSEYPPF SHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGSG
SYSVCSNSD TKTRTASGYGGTRRR
```

Signal peptide:
amino acids 1-30

Transmembrane domain:
amino acids 171-190

N-glycosylation site.
amino acids 172-176

Glycosaminoglycan attachment sites.
amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.
amino acids 98-106

N-myristoylation sites.
amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

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FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTACCTTTTGAAGGACAAG**ATGCATT**
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACCTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTATCCCCAAGAGCATCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCT**TGA**GAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGTAATTTCTGGAAGACACATC
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCTGGCCAGGATCTAAAACTT
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAAA
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAACACATCACGTAAAATG
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCGGAACTTTCTCATCTTGTAATTCTGAAGTTCTATAACCCACCGAACAACCTCCTCTT
TTCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGATTCT
GGAAAAGTGTTTCCTTCCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAAGTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTTATTTAACAAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLLYYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

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FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTTATTTAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCCGGAAGTTCTCCAGTAAAGTCCA
GACCTCTTGGAACCTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTCTG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAACTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACAGTTGAGGGATATTCAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCCTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTCAAGATTTTGAATCCAGTTATCATCAAAGAGAGCTGCCTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTTCAAGCCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAGACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAATAATTGGAAGGAGAGGGAGGTCACCTCTTTGATGGTGGCCCTGAACCT
CATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCCTGGAGGTCCCTGGTTCGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

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FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTTEECMDKMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGH TLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVIIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTP LHYFDSQCMAAMNFQTMHNVTTETKFLCLKLVKEGVVKDLSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

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FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCTTCCGCTCCAACATGG
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCTGGGTGCCAGTGCTCGTTATTGTCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTTAAATTTACA
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGACACATCTGT
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

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FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

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FIGURE 511

CAGCCGGGGCG**ATG**GCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCAGCCCCGTCCCACCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCAGGAGAGAGGAGCCTGTCAACCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCCGACACTGCTAGTGCCCCATCCCAAAGTGAGCATTTTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTTCTCCTGCCTTGGCTTGGGAAGCCT**TAGGA**ACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTTACTGGACGCTTCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCTCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTGTTTTATTAAAG
AGTGAATTTTTTAATTAAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAACTCGATCTCAGAGTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAAATGGCATATTTTAAATTTGGCCCAGACCAGAACCCAGTTTCTCTGGGATTAT
TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACTAACTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTTACCAAAATATTTAAATACTTTGACAGAAAAAAATCAAGCGAACTCTTT
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTAATAAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAATACTCTAGTGAACAAA
GACCTGTTTCAAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTTACATACAAGAGGTGTTGCGTTTCATTTTGGCGCTAATGTCCAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCAGCTGTTGGACCTGC
TGCTTAGAACACAGATTGGTACCTCGTGCC

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FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
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GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCCTGTTTCGGGCCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTTCAGCCCATCCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCGTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCTCCAGCTCAGCCACTGCAC
TGAGAACATCGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTCACCGGGGATGCACGGTCTGCATTTTCGGCCCCCTGCGGGACAA
TGGAGGCCTCTCTCCCTTTGTGCCGGGGCCCCGGGCCTCTGCAGACAGACCTCCATGCCCA
GAGGTCAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCAGTCCAGCTGACCCCTCAGTTCTTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCAG
TACACACAAGTTTCCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGCGCGCTT
CCAGCGCATCAACAGTGCAGTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCTC
ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCCTTCTGCCACCTCTTCTGA
TTCCCAGGACTCAGCCAGGTACCTCGCTGATTCTGCCCCCTTCCCAGCTGCAAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTGAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGGAATGCCATCTCGAGCCCCTACAGCTC
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCAGTCCAGCTG
ACCCCTCAGTTCTCCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCAGTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

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FIGURE 514

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGSHPFVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSTGGILLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSVIPAPFFPAASMDA
GMRRTRHGTSAPAAAAAAPPRSTLNPTLGSLLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

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FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGAGCGGGCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAAGAAAGACTGAAATTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACACATACAGGGAGAGTGAGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCACCCAGAACCCCAAGTTTACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
CTACTCAATCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTCACAAGGAGGGGAT
CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTACCCCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAAAACCTGAGGAGACCCAAGAGAAACGAAGGTCCTTC
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAGAAAGATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
TCCCACAATGCTGTCCACTACGGGAAGCATTTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACCTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT
TTAATGTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTCAATTTTCTAAAACCCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTAGCAGTCTGTGGCATATTAA
TCAAACCTGTTGAATTGTTTTCTTACACCTGGAAATCTTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

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FIGURE 516

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKFHMPEDVREKKENLLLSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKROGAKTVFNKFSNMNWPVDIHPLNKS LVKDNKWKKTETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRYYVEDKHKILYCEVPKAGCSNWKRILMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGIIYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVS KLCP
CLNYDFVGKFETLEEDANYFLQMI GAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTPLL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

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FIGURE 517

GGAACTTCCCAGGCACCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACC**ATG**CCTCTGTCCAGCCACCTGCTGC
CCGCCTTGGTCCTGTTCCTGGCAGGGTCCTCAGGCTGGGCCTGGGTCCCCAACCACCTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCCAAGTGTGGTTACCACGGGGCCCTCGCCCA
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCCTGGGCCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCCTGC
GAGAGGCAGCCTCCTCTTGAAGCTGAGGCTCTGGTACCACGGGCCTCTGGAGATGTGGCTGAACTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGCCGCACTCCGGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCCAGGCCAACTGTCCCCGGGACACC
ACCACTGCCAGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAATCGGGGGACCTGTCTG
ATGAGAACCCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGGAACCACCGTGCTGGTGGTCTCTGAGCGCCCTCTGGCCACGCCCTGACCACAGCCCGAACA
GTGCACAGGGCTCCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCCAAG
CCTCAGGCACCTCCAAGTCTGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCTACCCCTTCCAGATCCTCCTGGCCGGGCAGACAGGCCCGG
GGGGCTCGTGGGTCTGGACGACCTCATCTGTCTGACCACTGCAGACCAAGTCTCGGAGGTGTCCACCCCTGCAGC
CGCTGCCCTCCTGGGGCCCGGGCCCCAGCCCCCAGCCCTGCCGCCAGCTCGCGGCTCCAGGATTCTGCAAGC
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GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGCCACCTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGGCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTGGCGGTACGGCACCCAGGGCAACCGCT
GGCACGAGGCCTGGGCCACCCTTTCCACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTGAGGGGCTCC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGCTGCGGCCGGGGCCCTGCTGGGGCCCTAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGGCGGAGGCCAATGCTCGG
GCCATGCTGCTGGGGCCCCCAACAGACCATAACCACTGAGACAGCCCAAGGGCACTACATGGTGGTGGACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCTCCCTGACCTCCAAGGAGCACAGGCCCTGGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGAGCCAGGCACCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGCACGGCGGGCTTGCCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTGAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC
CCGGCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCAAGCCCCCTGTGGACC
ACACCCTGGGCACAGAGGCAGGCCACTTTGCCTTCTTTGAACTGGCGTGTGGGGCCCGGGGGCGGGCGCCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCTCCGCTTCTGGTACCACATGGGTTTTCTGAGC
ACTTCTACAAGGGGGAGCTGAAGGTACTGCTGCACAGTGTCTAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGCGGCACCAAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTAAGCCA
CTCTGGGCGGGCAGCCAGCCCTGGGGCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
AGCCTGCCCCCAGCCCGGGGAACACAGCCGACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC
TCATGCTCCTGGTGTCTGTTGGGACTTGGGGACGGCGTGGCTGCAGAAGAAGGGGAGCTGCCCCCTTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA
CCAGTGATCCGT**TAG**ACCACCCAGACAAGGCCCGCTTCTCACGTGACATCCAGCACTTGGTCAGACCCTAGCC
AGGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCTGGGCTTCCC
TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACCCCTGGCCCATGAGGGCCGCCCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAA

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FIGURE 518

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
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KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETLTLWQSTGPGWPGW
QELAVTTGRIRGDFRVTF SATRNATHRGAVALLDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPTGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPSSRLQDCKQGHLAGDLCPVPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRLLQWRRVSAQESQGSAAAAGHFLSLQRAWG
QLGAEARVLTPLILGPSGPSCELHLAYYLSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPIQTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSFPGGQGLWRRQANASGHAAGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQFACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMQVQAERAWRVFEAVAAGVAHSYVALDDLLQDGPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPPPPVDHTLGTEAGHFAFFETGVLGPGGAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKELKVLHSAQGLAVWGAGGHRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQPPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGGRRWLQKKGSCFFQSNTAATAPGFDNIFNADGVTLPASVTSDF

```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
 523-529;540-546;678-684;707-713;791-797;870-876;921-927;
 937-943;954-960;1036-1042;1071-1077

Amidation site:

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

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FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAAGTATCAGCTCCTGGCATCTGTAAGG**ATG**CT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAATCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTCTATAGAT**TGA**GACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

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FIGURE 520

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLSMLRTMTRLCFLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGRSADFWD
DGYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

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FIGURE 521

GATCAGTGTGTGAGGGAAGTCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTGTTGAAA
TAAGAGGAACFTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAACTTCCAGCTCCACTTTCCTATG
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCATGCTTTTCAGTTT
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTGGGAAGAGTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTTGGGATTTTGAATTTCTCAAC
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTTCAGGGGAAGATGGTATTGTGGTGTCTTCTCTGGGTCAGTGTTTTCAAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAAATGATCTTCTTGGTCATCCCAAAACCA
AAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTATGC
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCATGACCTCACCTGGTTCAGCACTACTCTATAGATGTGA
TTGGGTTCTCTGCTGACCTGTGTGGCAACTGCTATATTCTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAT
TTAATAAACTAGAAAAGATAGAAAAGAGGGAAATAGATCTTTCCAAATTCAGAAAAGACCTGATGGGGTAATCCTG
TTAATTCCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTTCTTTCGTTGTATTTTCTAGGTGCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC
ATGGATATAAAGAGGTAAAAAACTTAAATTCACAAAATTCAGTAAACCACACAAAATCAGGTAAGTGTTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
CTCATCTAGATGTCATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAAGGTGAACAGATATTTTGGGATTAGTAACTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAGAAGATTATATGTTTATCTTTAAAAATGATGAATACTCATAATCTTATCTC
TATAATCAAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAACGCTTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGTAATA
ATGTTTACACTAGTAAGCAAAATATGTTAATCTTCTCATTTTTTACTGTCTATATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTGAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAATATAAGTATTTTCTTGTGTATGTATACA
ATAAATATAAATAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

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FIGURE 522

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLLQLFCVCGFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLT LRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLSVLFHFWIQDYDYHFWEEFYKALGR
PTTLCETVGKAEIWLIRTYWDFEFPPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLGSLFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRLYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPVMGVPIFGDQLDNIAHMKAKGA AVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD
LTWFQHYSIDVIGFLLTCVATAIFLFTKCFLESCQKFNKTRKIEKRE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

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FIGURE 523

GGCTGCGGGGTCGGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCCGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTCGGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCTGTTCCTGGTCCCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCGGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCACTGGCTGGTGATGACATTCTGGCTTGTC
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATACCACCTGGCTGTGGGTGAAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGCTGCCCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCCAAAGGAAGGAGCTGACGCT
GTTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACCTTCTGACACCTGTGTCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA
TCACAGACCCACCCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTCT
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTATTTTATTTGAGGTTCTTGTACAAAT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAATGTCA

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FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSIQKELEAPHRGWLQLQEADLSAIRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQGASWTSIQTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGCLRKSCGIAGGDKTERRDSPRATDLAGKRTES
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTGNVSKI
NAAFGDNSPAYCPPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAATQGEGETPKEGADAVSGTQKGKTGGQQRGGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLISELEEPLEPKRELSHHAAVGVVWVSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

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FIGURE 525A

AGTGCCCTCTGTCAATTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTTCTGTTAAGACTGTCCTTGGGTCATTATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGACACAGTGTGTGTTTGGCGTGACATGTGCATGTGTGTG
TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG
TGCCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCCTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACCTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAACATTCAAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGACACAGGGAACCTCCCAGAGGCTGCAGGGCTTCCCTCCCAACCTCCAACGGCCCACTTGCTG
AGCCCGTGCTTATCTGTTCAAGTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
ACTCTGTGCCAGCTTGGTGCAAAGCCCTTGTGTGTGCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAAATCTAGATGGAAATGGAGGTACGCAGTGGAAA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTTCTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
TTCCTGGTTGATTTCCCCACTTCCCCACCCCCAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC
CCCATGAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTCTCTGCTGAAAGAGAGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTAAGCTGCTAATTACTTCTGATCATGCAGAAATAAAGCTACGTCCCTT
GAAATACACCAGGCAGCTAAACATAATCTTTGCGTTTCCGTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAAACAAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTGCTCCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCCATCAGGGTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGTCTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGGATGCAAAACATATTTAGATGGCACAATTTAGATGATTT
ATCAGTGCTAATATAGAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACTTACG
AGGGGGTTCGTTTTACAGACTATGATCTTGCATGATTTCCCAAAGATGCTCATTAAGTATATGGTGAAGTAGA
ATTTGAATACAGAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTTGGTTCAAACCAGCCTTTCTTCTTTCAA
ACAACCTCAGTGCAATTCATGGTTTTGGAAAATAAAGTTGATTTTGAATTCAGACAATAAGTGCATTTTTAATG
TTTATTCTTTTATCTTGAAAACTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAGCACTTCAAACAA
CACAGACAGTACAATGACAAATTGGAGATCAGCTCAATCTCGGCCCCCAATTTAATGCATTGCTGAATATTCTT
CTGAACATAGTCCATCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAACTCTTGACAGTCAACAATGTGCAATTTGGGTATTAAAGGCTCTGCAAGTTCTGCACCA
AATAAACCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGATTCACAGCA
GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCAATTGAGAAAACGAAGAAACACACAGGTACTTTAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTGGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCTTTTTTG
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTTACCATCGTGTTAATTTCTGCAGAGCA
CTTATTCAAGCATACTGCATTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCACTTCTGAAATGATCTCCTTAGAATAAATTCCCCAATTTGATTTGCTGGGTTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCCATTTTCTAAATGCTTACTATGACTGGTTTCCAACTACATTTTAAATCTTGTTCATCTGATAGGCCAAA
AAATGATATTTAATTTTTATTTGATTGATAATGACCTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT
GAAACATCTGTTCTATCCTTCGTCAATGTTCTCTCATATGTTAACTTTTCTTATTGATTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTTGTTGTCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTGAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGTTTATTTTGTGTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATTTCTCCATATTTGCTCTTAGCATTTTTTTTC
TTTTCATGTAACCTTTTGTCTTTTCCAGAAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTTC
CCAAATGGTGATTGAGCTGTCCATTTCCATATTTCCCTTATTAGAAATGACCACTATATTATGTTCTAAATA
TCTGCGTACTTGTGTCCCTTCTATAATCTCAGTTCATCTCTTTGAGCTATCTTTTGATTCCCTTTTTCAAACCAC
ACTGCTTTACTGAACGTGTCATCATCTTATACATTTTAACTACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGCTTTTCTGGTGGTTGTAAGATGTTTATTCTCTGGATAAACTTTAGAATCACTTTTTGTCTCCAAGGTA
AAATATATCCACATTGAGATCATACTGAATATACAGACTAATTCAGGAAAAAATGTATGCTTTTATTGCATTGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTATTTTTGGCTTTTCA

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FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTTAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTAAATAGTTTTCTATTATTTGGGTTTTCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTCCAATGTTTCATAACTGTTTTTATATTCTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

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FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLP LLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

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FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACCTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA
TGTAACCTTTGGCATTATCCTTATTCCGACTATGGCAATTCTTGGAAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

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FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYFYK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

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FIGURE 529

GCAGCCGGGTCCCACCAATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCCTACAACACTGAATGGAGGTCAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAACCCAGTGCCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTCGCCGTGGAGACTTTTTCTAC
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCGTGTCTCCTTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATTTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGCCCTCCTCATTTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCACGCCTGCCTGGCTGCCTTTCACCTGGGAGTGCTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTGAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTTACTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGAAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAGTTTTTGTAAATAAATTTCTAAATTATCA

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FIGURE 530

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVAVKLRRHVE
MYQWVETEEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRSNSMKTWGLRAAGWMMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFACVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE
```

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

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FIGURE 531

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTTCCCCCCTCTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTTCTCAG
TAAGACTTCACTGAGTGACTGTTTCAAGCCCATGATTTACCTGCAGTTTAAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTTCACTATTACATCCCCGCCTGTAGCCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

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FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGTSGIRSHQLSAGHLGL

Important features of the protein:

Signal peptide:

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

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FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCCG
TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCTCC
CTCTTCCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCTTGAAGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTCAGGCGGGAGCGGCCCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCCGATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAAAC
AGCACAAAGTGTTGGCATCGCCCCGGCGCCCGGACAGTCCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCTCCCAGCGACGGACGCCAAAGGGTCCCAGGGCCGCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCCTTGGGCTGTCTCCCGCGTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCAATTGTGCAGAAAAGTCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTCGTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 534

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMEN TAQLPECCVDVVG VNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPG EAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPI PAPP

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATCG**
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCTGC
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATGCTACTAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTCTCCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAAC
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTCGAGTTG
TGTCCTATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTTT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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FIGURE 536

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLFLLVVRVNEVNFPLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFNRMRKDGNGIVYNMLKKTVGIIY
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

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FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTGAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCAATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACTCCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTGAGGGTCCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAAAAGAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGAAGCCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAACTTCCTTATGTCCCATGGATCTCTCCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCCCTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

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FIGURE 538

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFKYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTTAGTTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

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FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLP LLPALVLSTRODYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNE DSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

FIGURE 541

CTCCACGAGGCTGCCGGCTTAGGACCCCCAGCTCCGACATGTCGCCCTCTGGTCGCCTGTGTCTTCTCACCATCGTTGGCCTGATTCTCCCCACCAGAGGACAGCGTTGAAAGATACCACGTCCAGTTCTTCAGCAGACTCAACTATCATGGACATTCAGGTCCCGACACGAGCCCCAGATGCAGTCACACAGAACTCCAGCCCACCTCTCCAACCCCAACCTGGCCTGCTGATGAAACACCACAACCCCAGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACAAGAGCACCAAAGCAGCTCATCCCCTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAAGCACAGACGTCCAGACAGACCCCCAGACCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCTTCTTCTATGATGAACACACCCTCCGGAAACGGGGGCTGTTGGTTCGCAGCTGTGCTGTTTCATCACAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGGTTATGCCGGAATCGTTGCAGGTGAGTCCATCAGAAACAGGAGCTGACAACCTGCTGGGCACCCGAAGACCAAGCCCCCTGCCAGCTACCGTGCCAGCCTCCTGCATCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACACAGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCCTGCCCGCCCCTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAAGTAAAGCACTGTGGTCTTTAAAAA

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FIGURE 542

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQOLEGTDGPLVTDPEETHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSKGKCRQLSRLCRNRCR

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

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FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTCTAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC
GCTCCGCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTCTAGGCTCATTCCCAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAAGGGTATCTCTCTCGACGGCAGACCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGT**TAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

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FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCQAHSQNVTFVL
RKVNDSGYKQEQSSAENAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

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FIGURE 545

GGCGGCCCCGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCAAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTTCGCGCATCGGCTCCGTCACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTATAAACTCGTTTAC
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTCGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAGGAGACGCTTCCTGTGAAGCCCTAAACCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

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FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81, NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLALLLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNLSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRRTTQVLVGGHHIPHPQDVEKQMQEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPITIRKEQRSDDYYHVLEAANEGDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNSGFKETLPVKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

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FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTCCTGTCTAGTCCAGGGTGTCT
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAACCTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGCCAGGGATCTCTGTCT
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGCTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCTCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCCGGCCCCCTG
CCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCTCTGATGGGTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTTGGCAGGGGGACAGGAGACTGTAACAGGCCAGGTCTTGTGCAGCCCCCTGAATGC
ACGCCCCGCTTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCCTTAGGACAAGGCAGACACCCACCATGCGG
GCCTCAGGTGGCAGAGAGGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTAGGCAGGCCAGCCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCACCCAGCACCCGTCCCAAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAAACT
ATGCATTTCATTAGCAATAAATGAGCCTTTGCTGCA

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FIGURE 548

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTQGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRRAQPTDSGT
YQVAITINSEWTMKAKTEVQVAEKNKELPSTHLPSTNAGILAATIIGSLAAGALLISCIAY
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPHLQAEPENHQYQQDLLNPDPAAPYCQLVPTS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCCTTCACCACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCACTGGGGTTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAAACCTCAGGAGTGAGAATTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACCTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACTTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTGCTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCACCTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTGTCATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTGACGA
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGACGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT
CTGTATAGTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCCTCGCAGGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCCTGTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCCGTTACAGTGGAGCGTTCCGTGTCCATAAAACGTTTCTAACTG
GGAA

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FIGURE 550

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPTARAGPGQAWSLRC
VLVGILHSDRRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

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FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
GACCCTGGCCCTGGGTACCTTGCCCTGCCTTCCTACCCCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAAGTGA
GCTGTTCCCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCAACAGCCTTTCTTTGTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCGCCGGTTGGCCTCAGCCCCATGCACCTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCACCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCT
ATTATGGACGGCAACTGTTATTACAAGAACCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCGCAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCCGCCTGCGACCACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCTCTACAA
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCCAAGCTTAACCTGTCCCTCAATTACCAAAA
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTCGGGAGCCTGGTTCGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTCCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCCCTGCCATGCTCCAGACTCTGCG
TCTGCAGATGAAGTTTCACTCAACAGGCCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTCAACGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA
CCTGCAGTGCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCAGTTCTTCCGCTGACCGG
TCTGCAGGTGTAGACCTGTCCCACAATAAGCTGGACCTTACCACAGGACCTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACCTTCAGCTTCGTGGC
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCACAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACCTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCGCCTGCACACCCTCCTGCCCCAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCCTGCCCCAACTGGAAGTCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTCACTGCAACAGCATCAGCTTCGTGGCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCCTTTATGGA
CTTCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
GGGCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTGGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCTGGGTGTGCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCTGCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGCGGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGA
GTGCCGTGGGCGCTGGGCACTCCGCCCTGTGCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCCCTCTTTGAGAA
CCTGTGGGCTCGGTCTATGGCAGCCGCAAGACGCTGTTGTGCTGGCCACACGGACCGGTGAGTGGTCTCTT
GCGCGCAGCTTCTGCTGGCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGGTGGTATCCTGAG
CCCTGACGCGCCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA
CCAGCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCTTCTATAA
CCGGAACCTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGAATCCTGCACGGTGCCACCTC

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FIGURE 552

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLP SLRHLNLKWNCPVGLSPMHFPCCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCYY
KNPCRQALEVAPGALLGLGSLTHLSLKYNNTVVPRLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRCDHAPNPMCECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFYKCIKTKALQGLTQLRKLNL SFNYQKRVSFAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGEKVLQPGDLAPAPVDTPSSEDFRPN CSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFQMGVGHNF SFVAHLRTLRLHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWL DLSQNLRLHTLLPQTLRLNLPKSLQVRL
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNL SANALKTVDHSWFGPLASALQILDVSANPLHCACGA AFMDFLLEVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGV PMLHHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEALPYDAFVVF DKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLL
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE
Important features of the protein:
Signal peptide:
Amino acids 1-30

Transmembrane domain:
Amino acids 818-835

N-glycosylation sites:
Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735

cAMP- and cGMP-dependent protein kinase phosphorylation site:
Amino acids 347-351

Tyrosine kinase phosphorylation site:
Amino acids 863-871

N-myristoylation sites:
Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016

Amidation site:
Amino Acids 974-978

Leucine zipper patterns:
Amino acids 204-226;644-666;814-836

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FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGCGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCGGGGTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCCGGCGCCCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTCCTTGGAAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTGGGAGGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGGACACTTCAAGTTCTGC
ATTACTTTATTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAACGTCCTTAATTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFTNLSLQNNITIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFGEGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCC**ATG**CCTGTTTTCTGGAACCAGTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGAAGTCTAACCAGGTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGGTCTCTGCGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCAGATGCACC
TACTGCCCTCACCACCT**TGA**ACCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGCAGCGGAGTTACCCGTGTGGGTTCTCTG
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTCGCCAAGACGAGTCCGACGCCCC
GTGGTCAGTGTGTTGGGGCCAAATGCACGGCGGCCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGCACCCCCGTGCCCCCTCCGCGCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
CCTACCCCTTGCCCTTGCGGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTGCGCGCCGTGGGCAACTGTTGGTTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTGAGCCTTTTCGCCACCCGCGCGCCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCCTCTGCACTTCAG
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGGACAGTCCTTCCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCGGGCACCAAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCACCCCTGTCTTGAGCCCGTCTACCAAAATAAAGTTGTAG
TGATTCCA

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FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLLELGHVLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHRGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALTT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

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FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGTGGTCAGACCCGCTTATGTGTCAGCATTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTGACCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTTCGACCATTTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

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FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLLRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVSVLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

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FIGURE 559

CCCAGCCCCGCGTTCTGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCGCCCCACGCCCGGATGCTCACCCCTGGATGCCAACCCCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCTTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG
AGGCTGGACTTGTCTAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCCCTCAACGTCAGCTACAACGTCCTGGAGTGG
TTCTTCGCGACCGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG
CTGCTGTTCTTCCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCTGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC
GGCTTCTGAGGAAAATGCCTTCCCTCTCCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTCCGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTTAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCAATTGCCAGACTGCCCATTTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGGAATTGCTTGACCACCTTCCCCAAGTTTGGGGG
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG
GTCCGCACACAACAGGACACTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCACCCACCCCGG
CCCCACCAACCGCCCAAGTTCTTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAT
ATTTATTAAGTGACTTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
AAAAAAAAAAAAAA

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FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTVGWRNRSGTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEGL
ERLRELDLQARNYIFEIEGGAFDGLAELRHLNLAFFNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRITLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTVSLWEEFSSSDLDLRLDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHPLASCLGSLRLFNLSNQLLGVPFG
LFANARNITTLDMSHNQISLCPLPAASDRVGPPSCVDFRNMASLRSLSLEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFPRFGGSLALETDLRLRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIIPSC
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSV

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

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FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC
TTGGGCTGGAAGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTA
TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAACCTTGACCTGTGCCTGAGCCCGAGGCATTGAGAGCTGATT
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTCATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTACTACTAAGCTGCCTTGGCAGTTTGCATTTTTTGAGCC
AAACAAAAATATATTATTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELD PVP
EPEAFRA DSE DGE GAFSE STEGLQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK
LKVP GSE SRTGNSSPASVEREKTDAYKVLKTEMSQ RSGGQCVIHYSKGFRWHQNL SLFYK
DCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

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FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGGCTGGGTGAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

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FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSI TLGRYLRLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

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FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCAATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATACCATTACTGCTGCTACGTCGTTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCTTCCTATCCACTGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

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FIGURE 566

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIPLLLRRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

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FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCAATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

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FIGURE 569

GGTGCCAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTGCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGGCTGGCAATCTTCTGTAT
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCCTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTGCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAGAAAGAGACCGAAAGCAAAGTCATAAACC
ATGCCCACGAGCTCAGCTGTCTCTGCTCCGTGTCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCTC
TGCTACTTCTCTGATCCTCTCTTCTGTGTCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCCCTTACC
AACCCCTCTGGCTCCCAAACTGCCACTGTACGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAAACTC
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGCTCTAAGGCTCCAAGAAAGG
TTACCCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATAAATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCCACCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTCCAAAATAAAAGAGAATCTTTTCTTCCCTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFSDVKLYDLLEFTNSPFQDFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQESECYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDYFRHLESELAKTESTYLAEMHRQ
SPKEKASKTTTTVRRRKRPAAHLRVPHLEEVMSPVTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLEFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQOKYHDELQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

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FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTCCTCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAGGGGAGTTTGGAAAGGTATGCATCGTGCAGAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTTCCAGGTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCCTCCACGTGGTGAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAAGTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGGCTTTGTGCCCAATAAAGGGAGGTTGAAGTGGGATCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAAGACAGATCCAGGGATGGCACAAGGACAGCTG
CCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTCAACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCCACTTGTGT
CTGCTCAACAGGACTGCACCTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCAATTAGGTAGGAAACATGAAAAACCTTTGA
TATTTATAAAATCAATTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCATTCGCCAAAGCAATCAA
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCTTCTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGATTCTCTGGCAGGCCACAGTCCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCCT
CACCACCACCATATCCCAGTGCTGGGATGGCACACAGGTGCCATTAGATGAGAGTTGGGTCGCTGAGCATTTG
GTTACTCCTGCAGAGTGTAAATCAGCACCCCATCCAAGTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTTCAAGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTTACACAAAAAGCAAACTACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAACTGGAAGA
TGTTGGGATGAGCAGGGAAGCTTAGACTTTGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAC
TAAGTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATATCGTCATCATATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTT
TGTGCAAAACAACCTGTTTAGGATTCTTCCAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
TGAAGTTCGACTGTGTTTTTATTTTTTTCATCCAACCTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCATCTTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTATATTTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTTTCTTCTTCAACCCAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGACACTTTTTTCTTACTTCATGTCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTCTGTTCAGTTGGCATTCTTGTGTTG
GAATAAACTATTTCTTGG

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FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLGGDLRY
HLQQNVHFTTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGRLNCDPTFELEEMILESKPLHKKKKRLAKNRSRDGTDSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

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FIGURE 573

CTCCAGTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAAATAAATAAACGTC
CTGAAC TGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGCGCAGAGG
AGACCTCAGCATCATCTAGAGCCAGCGCTGGCCCTGCCTCCGCTGCGCCGCCGCCGCTCGCCGTTTCTGTT
CCTGCTACTGTCCCACTAAACAACCTCCCGTTACACGGACAAGTGAACATCTGTGGCTGTCTCTCCTTTTCTTC
CTCCTCTTCCAACCTCTTCTCCTCCTCCACTTCCCAGCCGAGCAGAAAGCCCCCAACCAACTGACGCTGGCA
CAACTGCAAACGGTGTCTATCCGCACAACCTTTATCTCGCTCCTCGGGCTCCCCTAAGGCATTTGGACCCATCGCCGC
GTCTTTTATTTTGCAGAGTTGCATCGCTGTACATATTTTGTCCCCGCCACCTCCCTCTGTCTCTGGAGTGCC
TACAGCCCCGCAAACTCCTCCTGGAGCTGCGCCCTAGTGCCCCCTGCTGGGCAGTGCGCTTCCCCCCCATCCTCCC
GCGCCAGCCCCCTGTCTGTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCGAAGCGCCTGAAAAGGAGAGACAGGAGGATGATGTCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGGTGGCTTCTACCTCGGCTGTCTGCTGCTGCGGAGTGACAGCCCGGGGCTAGGGCGCCTG
GAGAATAAGATATTTTCTGTTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCATTGTG
TCTCCACATTTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGAAAGAGACCTAGTACTTCTCTGTCTC
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAAC TGCGGAT
GAGTTTTGCTTTTACTATGCAAGAAAAGATGGTGGGTGTGCTTTCCAGATTTTCCAAGAAAACAAGTCAGAGGA
CCAGCATCTAACTACTTGGACCAGATGGAAGAATATGACAAAGTGGAAGAGATCAGCAGAAAGCACAACACAAC
TGCTTCTGTATTCAGGAGGTTGTGAGTGGGCTGCGGCAGCCCGTTGGTGCCTGCATAGTGGGATGGCTCGCAA
CGTCTCTTCATTCTGGAAGAAAGAGGTTATGTGAAGATACCTTACCCCTGAAGGAGAAATTTTCAAGGAGCCTTAT
TTGGACATTACAAAACCTTGTTCAAAGTGGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCAT
CCCAATTACAAGAAAATGGAAGTTGTATGTCTCTATACCACCAACCAAGAACGGTGGGCTATCGGGCCTCAT
GACCACATTCTTAGGGTTGTGGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTGAGAACAGCCAGA
GTCTTTTCTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAACTGCTCTTTGGCCCTGACGGCTTTTGT
TACATCATTTCTTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTAAAGTATTTACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCCATACCAAGGAGCAACCCACACTTC
AACAGCACCACAGCCCCCGAAGTGTGCTCATGGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCCTGATATAAACATCAATTTAACGATACTGTGTTTCAAGTCCAATGGAAAAACAGATCATCAGCCAGAATT
CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTAGAATTCAAGCCATTCAGTAATGGTCCT
TTGGTTGGTGGATTTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTTAACCTCTCCAGCAAAGTCTGTGACAAAGCAGTGGAAGAAAAACCACTCTGTCTCGGCACTAGT
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTTGGAGAAGATGAAC TAGTGAGTTTACATTTTA
TCAAGCAGTAAAAGTATGACCCAGACTCACAATGGAAAACTCTACAAAATTGTAGATCCCAAAGACCTTTAATG
CCTGAGGAATGCAGAGCCACGGTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTCTGTGCAACCGGC
TACTGCACCCCCACGGGAAAGTGCTGCTGCAGTCCAGGCTGGGAGGGGACTTCTGCAGAACTGCAAAATGTGAG
CCAGCATGTCTCATGGAGGTGTCTGTGTAGACCGAACAAGTGCTCTGTAAAAAGGATATCTTGGTCTCTCAA
TGTGAACAAGTGGACAGAAACATCCGAGAGTGACCAGGGCAGGTATTCTTGATCAGATCATTGACATGACATCT
TACTTGCTGGATCTAACAAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT
TTTTTATCCTGTCTATTAATAAAAAAAAAAGACTGTTATCCTGTCTACACACTCCTGTGATTTTCTCTTTTATTA
TTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTGAGCATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTTGCATAACAGATGATTTTTTAAATATATACTTCTTATGCAAAGTAAT
TTACACAGAAATTCATTGTAAATGATAATGGATTTTTTATGTTACTAGAAGAGATTATTTGACTTCCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCAACTTTAATAGAGTTTTGAAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAAGCAATATTTTTATATTAAGTACTATATACTAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATGTAATCTTCATTTTTGTGAGTGATCCAGTTACAGAAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTCTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT
AATAGCATATTTTAAATCAAAA

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FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRCVRSRQRRPQHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLLPLPSRSRKPPPTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVIFYCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMSQ
LELLSGGEMLCGGFYPRLSCLLRSDSPGLGRLENKIFSVTNNTCEGKLLLEEIKCALCSPH
SQSLFHSPEREVLERDLVLPCLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEDYKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNKG
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVDVTDMCNVPYSIPRSNPHFNST
NQPEVFAGHLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEEP
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLGPQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

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FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCTCT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGAACCTGCAGTTCTGCCACACA
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATTC
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCACACGTGGAAGTCTGATACCGCTTGCAGAAGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCGCAAGCAACAAC
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTCAGACACAGGGGAAACC
ACTGCCTCTTTTCACTCTTTCTCCAGATTCCAACAGTCACTGTTACAGCATTTTCACTTGTTC
ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCAGATGCACATCTGGTGTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCTGTCAGTCACTGTGTCAGTCCCTGAGGAGCCTCCTCA
CCGCTCTTCTTTAGTTTCTTCACTCTGTATAGACCTGCCAGAGCAGCTCAGGGTGGAGGAT
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCATCAACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACATCATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTCACTTTCTTGATACCGTCTGGGAGGATTG
CTGGCTGGTTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTTCAGGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCTGGAGAAG
TTCACTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGCAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATAA
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTGTAACCAGAGACCGCTTGGCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTACAGCTGTTTCTGATAAGCACTTGTG
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAAACAA
CCCATTCTGCTCTCCTCTTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
CTAGAAAAGCTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTGTCTCT
GAGATAAGGAGGAACTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGTGCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTTGAGCCTTGGGGGACCAGTTACCCCTACATCCAGGCTTCTGTTGTCCCTTGCCCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFFPSLVSCVQVPFSWIPCLECFIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

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FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAACTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTGAAGAGGTACGCAGGAAGTATATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATTAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTCCATCTTTGATTACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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FIGURE 578

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

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FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTCACAGTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTTTGAAACAGCCATTTCTTCTTTTTGGCAAACTGAAGAGGGTTCAC
ACAACTTATTTTAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCAFTCTTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

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FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVQLPPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNNKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

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FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCCCTTGTGTGTAGGGCCGCCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCCAG
GGAAATCTCCGACCAGGCCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTTCCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCTTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTGAGGAGCTGGAGTTGTCCTTGCAATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACCTGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCCTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGATGACTGCCTTTG

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FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFLEYLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVEYEFDEVMPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLETFPRIVFMLGFVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

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FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTGGACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCTCTCTTCTGCTTCAGAGGGAGAGCAGGCCCGTCGCCCCATTTCCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCACTGGACTAAGAGTGGG
CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTGAGGCTACACAAGCAGGCCCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT
CTGGTTGCTGGAGTTCTCGGAACCTGACATGTGCGAGCCGTGGGGATGCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
GAGAGCACCTTAACCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCGGAGCCAGGCC
CTGCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCACTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCCTGTGCCAGGCCACAGCCCAGCCTCCTGTACAGGCTACAGG
TGGCAAAAGGGGGCTCTCCGGTGTCTCGGGGCCCGCGGGCCAAGGTTAGAGGTCGTGGCAGACGCCTCGTTCCCT
ACTGAGCCCGTGTCTCGGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCGGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCCTTCAGCTGCGCCTGG
CGCGGGAACCCGCTTCCACGGGTAACTGGACCCGCCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCGAGGCACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCCTGCCG
GGCGGCGCCGCGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCCCTGCACTCTGCGCCTGCCCTTC
CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGGTTTTCGCCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTGGAGGCGGGTTCGAGGGCCGTTCTTGGTGGAGACATTCCTGCCCCAGAGAGCCGCGGGGGA
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCGGTAGAGACTTGCTGCCCACTGTGCCG
ATAGTGGCCGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGTGGCGC
CACAGCAAGGCCCTCAGCCTCTTTCTCCGAGCAAAGAACCTGATGCCAATCCCTGGCAGCAGCGACGGCTCCAGT
TCACGAGGTCTGAAGAGAGGAGACAGGCAGCCGCGAGGACCCGGGGCCCCATTGTGCACACTGACCACAGTGAT
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCCAAACCGTTACTACAAGTCCGAGGAGTCAGT
GTGAGCCTGAGCCTTGGCGAAGCCCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCCAGGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTCACCACACCCCAACCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
CCCGGGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCGTCTCCAGACTCACGTGTGACAT
CTTTCCAATGGAAGAGTCTTGGGATCTCCAATTGCCATAATGGATTGTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCCTCCAAACTGAACACAAGGGGAGGGAAAGATCATTACATTTGTGAGGAGCATTGTGATA
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCAACCTGGCTCTCCCTGAGGGGAACCTTTGCTCGGCCAAT
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTCCCTTAA
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAATATTGGGATAA
AAATATTTATGTTTAATAATAAAAAAAGTCAAAGAGAAAAAAA

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FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGSPHFLQOPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHLHIRPVELEDEASYECQATQAGLRSPALHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSPVESTLTLPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPASPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSFVLGARGPRLEVVDASFLTEPVSCEVSNVAVGSA
NRSTALDVLFGPILQAKPEPVSDVGEDASFSCAWRGNPLPRVTWTRRGGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEEARLTVNAPPVVVTALHSAPAFLRGPARLQCL
VFASAPDAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHSKAS
ASFSEQNLMRIPGSSDGSSSRGPEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTPHPRAFTSYIKPFSFGPPDLAPGTPPPFYAAFPPTSPHRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

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FIGURE 585

CCCCGCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG
CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCAGAGCCGCCAAGGAAGAGAAA
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAACCCCTTCCA
GCTCGATCTGCTCTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
ATGCTGTCTGGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTGAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCTCACAGTCTGCTGGTGCCGCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTCGTGCCACCAACAAAGCCATCCCGG
AGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACTTTCCTACTGCTCTGCAAAGGCCAACCAGC
TGTCACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCCTGAGCAATGAGAAGACCCTG
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCCCTGGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
TATACGGTGGAGACCATCAGCACCAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTCCGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTATCATTTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCTGTCCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCGTTCCCAGAGAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCCCTAACAGTGTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA
CCTGGACTAGACTGAACCTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAACGTACAGAAAAGATAGGGGGAAAAGCGGTTTGTGTTTGTATCCTTGCTCTAC
AAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAAACCTAA

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FIGURE 586

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLFLFVCFFLFSQELGLQKRGCCCLVLGYMAKDKFRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFIISPGDVENGQSIVCRATNKAIPGGKET
SVTIDIQHPPLVNLVSEVPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLVDLGSDAIFSCAWTG
NPSLTIVWMKRGSGVVLVSNKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLESSTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQSGSEMKGAGLEAESVPMAVIIGV
AVGAGVAFVLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 587

CAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAGAAGCATCAGAAAGCACAAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTGAGAAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAATCCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

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FIGURE 588

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEESESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLMSWLVCCKSL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

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FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCGCTTTTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCCAGGGTGCCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTCACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTA CTCTCTGCTCCGCCGGCCGTTT
CGCCAAGTCTTGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCCTGCAGCAGACACACTTGA
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLGHLLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRM DVTMKALALLADLHPSVRQRCLIQKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

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FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATAACCAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTGTTTGTAT
GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAAACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAAGTGAAAACAACAAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAGAAATGACTCTA
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACCTTGATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGTATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTCACTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
ATACTAACACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAGAAGATGATGATGATGCATTAGTC
CCAGATAGCAAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTCAAGGAATCCAAGAGGGGCCCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAAACAGAGCCCATAAACTATTGACCTCTGAGG
TTTCATTGGAAAGAAAGTGACTGTGCATTATCCATTACAGTAAAGGATTTTATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTCCCTAAATAAAAAATCACCTTTTAAGCTAGAG
CGTCCTTACAACTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTGTAGTGTACACCAGCTGAATACGGAGCAATGGTGTATAT
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

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FIGURE 592

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPLPWRVPGQLDPSTGRRFSEHKLCADDECMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYKLRGWPEVWAGSVGRFTGYFPKDLIQVVHEYTKHEELQVPTDET
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSENTEDLQEQFTTQKHSHANSQANHAQGEQASFESEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTGFGSTADALVSDDETTRLVTSLED
DFDEELDT EYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDTMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

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FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACA**ATG**TCTGAAGAAGTGACCTACGCGACACTCACATTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTTGGCG
TCATGCTGCTCTGGGTCTGGTAACCTCTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCTACTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGACGT
CTCTAACTAT**TGAG**GGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG
CGAATTCTGCA

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FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80, NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINS DSEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNPCPKMWQWYQNSCYFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

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FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAATTTCAAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTTTCGTAACCTTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCTTCTTGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWI SRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMEDESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLA FQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHGASKGRCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

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FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGGCTGAAGAGGG
ATTCACAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCTTGGGGGGGGG
CAGCĀCAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAGATGCCCTGTGCCCTGGTTCTT
GCTGTCTTTGGCACTGGGCGGAAGCCCAGTGGTCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCTGCTCCGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCAATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCCGCTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCCAGGTACGAGAAGGAACCTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGCTGTGAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCAAAACCCCGGTGGCACAAAA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCTGCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTTCAAGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCCGAGAAGCGGCACTGTGCTGGCGGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTCCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAGGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGGCGGCCGAGGGGCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTGGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTCGTGAAGTGAAGCGCAGGGGCCCCGTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCCGGGGCGCACGGCCCCGCACGACGCTTCCG
CGCTCGCTCAGCTGCGTGCTGCCGACTTCTTGACAGGGCCGGGCGCCCGGCAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCACCGTGCCCGT
CTTCACACTGCCCTCCCACTGCCAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACTTAAATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 598

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLRLVGPQDATHCSPGLSCRLWSDILCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFQAYPTARCVLLEVQVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALFVLNVVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPGQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQEQECLWADSLGPLKDDVLLLETRGPQDNRSLEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSLLL
LKKDHAKGWLRLKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWFAQRRTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLLHPDAVPALFRTVPVFTLPSQLPDLGLG
ALQQPRAPRSGRLOERAEQVSRALEQVSRALQALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

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FIGURE 599

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTTCAACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCACTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCCTCAGGCACAACCCAACTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCT**TGA**GGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCAATAGCTCATTCACTGCCTTGATTCTTTTGGCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTGAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCTTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAA

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FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTF
YDCGNKTVTPVSPGLGKKNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCCCTGACA
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA
TAGATGTCAACAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

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FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCVLVLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPD SGKAWLWMDGTPFTSELFHIIIDVTS PRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVP PETLGEGD

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FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAAT**ATGC**ATCTTGACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCCGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 604

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 605

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATGG**
TCCCCGGCGCCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGT**AGAAGA**
GTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCTACCCAGGGTCTCTGCACAGTGACCTTACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI

HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSFYV

EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCCATGTGGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
AACCTCTGACTAAAGACATGGCCACTTAGAGAGATGGATCTGCAGAGCCTTCCCTGCCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGA
GAGATAGGGGCCCTGGGCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTCATAGGAAAC
CTCTCTGATCCACACACAAGGAGGGTGATTCTGGGATGAGTTCTGGTCTTAGGGCATGAGG
GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCCGGCCCGGTGCTTGCTCCTCCCCCTCCACCTCTTCTCCTCCTAGCT
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTGAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACGTGCTTAGGGAAGTGGTCTGTCTCCTCACAGGCTTACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCACCTGCCCACAAGCAAACACACCACACATGTTTCGGC
ATGTTGCCCTTTGAACACCCATGAGGACGCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGTCTTTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCCATAATGGCCAGAGAGGAGAGTTTCAGCCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TGGAATGCTTTCTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTC AACGTGATGTCATTCTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC
CGTCAATCTCTCTGGGAAA

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FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGS�TVQCHYKQGWETIYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRFTFTVTMEGLRRDDADVWCGIERRGPDŁGTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMFSEPLTKDMAT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

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FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTGATTTCTCCCCAGTCCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACCTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATAAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAAGGAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTTATTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT
ACAGTAAAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTTATTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSELTIKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142

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PCT/US00/30952 8 November 2000 (08.11.2000) US
PCT/US00/32678
PCT/US00/34956 1 December 2000 (01.12.2000) US
20 December 2000 (20.12.2000) US
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| PCT/US00/05841 | 2 March 2000 (02.03.2000) | US |
| 60/187,202 | 3 March 2000 (03.03.2000) | US |
| 60/186,968 | 6 March 2000 (06.03.2000) | US |
| 60/189,328 | 14 March 2000 (14.03.2000) | US |
| 60/189,320 | 14 March 2000 (14.03.2000) | US |
| PCT/US00/06884 | 15 March 2000 (15.03.2000) | US |
| 60/191,048 | 21 March 2000 (21.03.2000) | US |
| 60/190,828 | 21 March 2000 (21.03.2000) | US |
| 60/191,314 | 21 March 2000 (21.03.2000) | US |
| 60/191,007 | 21 March 2000 (21.03.2000) | US |
| 60/192,655 | 28 March 2000 (28.03.2000) | US |
| 60/193,032 | 29 March 2000 (29.03.2000) | US |
| 60/193,053 | 29 March 2000 (29.03.2000) | US |
| PCT/US00/08439 | 30 March 2000 (30.03.2000) | US |
| 60/194,647 | 4 April 2000 (04.04.2000) | US |
| 60/194,449 | 4 April 2000 (04.04.2000) | US |
| 60/196,820 | 11 April 2000 (11.04.2000) | US |
| 60/195,975 | 11 April 2000 (11.04.2000) | US |
| 60/196,000 | 11 April 2000 (11.04.2000) | US |
| 60/196,187 | 11 April 2000 (11.04.2000) | US |
| 60/196,690 | 11 April 2000 (11.04.2000) | US |
| 60/198,121 | 18 April 2000 (18.04.2000) | US |
| 60/198,585 | 18 April 2000 (18.04.2000) | US |
| 60/199,654 | 25 April 2000 (25.04.2000) | US |
| 60/199,397 | 25 April 2000 (25.04.2000) | US |
| 60/199,550 | 25 April 2000 (25.04.2000) | US |
| 60/201,516 | 3 May 2000 (03.05.2000) | US |
| PCT/US00/13705 | 17 May 2000 (17.05.2000) | US |
| PCT/US00/14042 | 22 May 2000 (22.05.2000) | US |
| PCT/US00/14941 | 30 May 2000 (30.05.2000) | US |
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- (74) Agents: **BARNES, Elizabeth, M.** et al.; c/o Genentech, Inc., MS49, 1 DNA Way, South San Francisco, CA 94080-4990 (US).
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- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

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INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/06520

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C12N15/62 C07K14/47 C07K14/705 C07K16/18
G01N33/53 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, SEQUENCE SEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 63088 A (BAKER KEVIN ;CHEN JIAN (US); GENENTECH INC (US); YUAN JEAN (US); G) 9 December 1999 (1999-12-09) page 1 -page 2; claims 1-26; figures 3,4; examples 1-3,5,139-147 page 281 -page 284 page 305 -page 314 page 345 -page 373 ---	1-24
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

- "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- "&" document member of the same patent family

Date of the actual completion of the international search

28 February 2002

Date of mailing of the international search report

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Oderwald, H

INTERNATIONAL SEARCH REPORT

Internatic Application No
PCT/US 01/06520

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
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P,X, L	WO 00 73454 A (GENENTECH INC) 7 December 2000 (2000-12-07) page 1 -page 2; claims 1-118; figures 3,4; examples 1-3,5,139-172 page 43 -page 44 page 283 -page 288 page 304 -page 316 page 338 page 371 -page 398 ---	1-24
P,X	WO 00 58473 A (CURAGEN CORP ;LEACH MARTIN (US); SHIMKETS RICHARD A (US)) 5 October 2000 (2000-10-05) see SEQ ID NOs: 3231 and 3232 (pp. 2436 and 2437) page 1 -page 4; claims 1-32 ---	1-24
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/06520

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 20 and 21 are directed to a method of treatment of the human/animal body (in so far as in vivo methods are concerned), the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this International application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-24 (all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-24 partially

An isolated nucleic acid SEQ ID NO: 1 which encodes amino acid sequence SEQ ID NO: 2. A vector, a host cell, a process for producing a polypeptide, an isolated polypeptide encoded by said nucleic acid. A chimeric molecule, an antibody, methods for stimulating the release of TNF-alpha, for stimulating the proliferation or differentiation, for detecting the presence of tumor, an oligonucleotide probe.

Inventions 2-305: claims 1-24 partially

same as invention 1 but comprising the polynucleotide and amino acid sequence in the order given in claims 1 and 2 (invention 2 is limited to SEQ ID NO: 3 and 4 and invention 305 is limited to SEQ ID NO: 609 and 610).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 01/06520

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International Application No

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